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(54) Title: 57242, A NOVEL HUMAN G PROTEIN-COUPLED RECEPTOR FAMILY MEMBER AND USES THEREFOR

(57) Abstract: The present invention relates to methods and compositions for the diagnosis and treatment of metabolic disorders, including, but not limited to, obesity, diabetes, hyperlipidemia, overweight anorexia, or cachexia. The invention provides isolated nucleic acids molecules, designated 57242 nucleic acid molecules, which encode novel G protein-coupled receptor family members. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing 57242 nucleic acid molecules, host cells into which the expression vectors have been introduced, and nonhuman transgenic animals in which a 57242 gene has been introduced or disrupted. The invention still further provides isolated 57242 proteins, fusion proteins, antigenic peptides and anti-57242 antibodies. Methods of use of the provided 57242 compositions for screening, diagnostic and therapeutic methods in connection with metabolic disorders are also disclosed.

**57242, A NOVEL HUMAN G PROTEIN-COUPLED RECEPTOR FAMILY  
MEMBER AND USES THEREFOR**

**Related Applications**

[0001] This application claims priority to U.S. provisional application serial number 60/228,409, filed August 29, 2000, the teachings of which are incorporated herein in their entirety by reference.

**Background of the Invention**

[0002] G-protein coupled receptors (GPCRs) are proteins that mediate signal transduction of a diverse number of ligands through heterotrimeric G proteins (*see, e.g.*, Strader (1994) *Annu. Rev. Biochem.* 63:101-132). GPCRs are a component of many modular cell signaling systems involving, *e.g.*, G proteins, intracellular enzymes and channels. Upon ligand binding to a GPCR, intracellular signal molecules, *e.g.*, G proteins, can be activated or turned off. These GPCR-coupled G proteins can modulate the activity of different intracellular effector molecules, *e.g.*, enzymes and ion channels (*see, e.g.*, Gutkind (1998) *J. Biol. Chem.* 273: 1839-1842; Selbie (1998) *Trends Pharmacol. Sci.* 19:87-93).

[0003] GPCR polypeptides typically include seven transmembrane domains, including an intracellular domain and an extracellular ligand binding domain. The intracellular domain(s) bind G proteins, which represent a family of heterotrimeric proteins comprising of  $\alpha$ ,  $\beta$  and  $\gamma$  subunits. G proteins typically bind guanine nucleotides. Following ligand binding to the GPCR, a conformational change is transmitted from the extracellular GPCR ligand binding domain to the intracellular domain-bound G protein. This causes the G protein  $\alpha$ -subunit to exchange a bound GDP molecule for a GTP molecule and to dissociate from the  $\beta\gamma$ -subunits. The GTP-bound form of the  $\alpha$ -subunit typically functions as an effector-modulating moiety, leading to the production of second messengers, such as, *e.g.*, cyclic AMP (*e.g.*, by activation of adenylate cyclase), diacylglycerol or inositol phosphates.

[0004] GPCRs are of critical importance in cell signaling systems, including the endocrine system, the central nervous system and peripheral physiological processes. The GPCR genes and gene-products can also be causative agents of disease (*see, e.g.*, Spiegel (1993) *J. Clin. Invest.* 92:1119-1125); McKusick (1993) *J. Med. Genet.* 30:1-26). G-protein mediated signaling in adipose tissue is known to be important for adipocyte differentiation,

metabolism and the regulation of metabolic rate and consequently for the development of obesity and/or diabetes. The most well characterized pathway is the adrenergic pathway which regulates both white fat lipolysis and brown fat thermogenesis/proliferation by modulating the levels of intracellular cAMP. Beta-3 adrenergic agonists, which increase cAMP in brown and white adipocytes, cause weight loss and protect from obesity in both rodents and primates (Yoshida et al., Eur J Endocrinol 131:97-102 (1994), Fisher et al., J Clin Invest 101:2387-2393 (1998)). On the other hand, overexpression of the alpha2-adrenergic receptor, which decreases cAMP, in brown and white fat of the beta3-adrenergic receptor knockout mouse promotes diet-induced obesity (Valet et al., J Biol Chem 275:43797-34802 (2000)).

**[0005]** While the cAMP-mediated signalling pathways are most well characterized, roles for GPCR-mediated  $\text{Ca}^{++}$ -signaling in adipocytes are also likely. For example, increasing intracellular  $\text{Ca}^{++}$  levels by either  $\text{Ca}^{++}$  ionophores or by activation of the alpha1-adrenergic receptor potentiates the thermogenic action of beta3-adrenoceptor-generated cAMP in brown adipocytes (Zhao et al., J Biol Chem 272:32847-32856 (1997)). Furthermore, GPCR-mediated increases in intracellular  $\text{Ca}^{++}$  have been implicated in adipocyte differentiation (Shi et al., Physiol Genomics 3:75-82 (2000)), lipolysis and lipogenesis (Xue et al., FASEB J 12:1391-1396 (1998)), and insulin signaling (Gonzalez-Yanes et al. Diabetes 49:1288-1294 (2000)).

**[0006]** Given the important biological roles and properties of GPCRs, there exists a need for the identification and characterization of novel GPCR genes and proteins as well as for the discovery of binding agents (*e.g.*, ligands) and modulators of these nucleic acids and polypeptides for use in regulating a variety of normal and/or pathological cellular processes.

#### Summary of the Invention

**[0007]** The present invention is based, in part, on the discovery of a novel human G protein-coupled receptor, referred to herein as "57242". The nucleotide sequence of a cDNA encoding 57242 is shown in SEQ ID NO:1, and the amino acid sequence of a 57242 polypeptide is shown in SEQ ID NO:2. In addition, the nucleotide sequence of the coding region is depicted in SEQ ID NO:3.

**[0008]** Accordingly, in one aspect, the invention features a nucleic acid molecule which encodes a 57242 protein or polypeptide, or a fragment thereof, *e.g.*, a biologically active portion of the 57242 protein. In a preferred embodiment, the isolated nucleic acid molecule

encodes a polypeptide having the amino acid sequence of SEQ ID NO:2. In other embodiments, the invention provides an isolated 57242 nucleic acid molecule having the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. In still other embodiments, the invention provides nucleic acid molecules that are substantially identical (e.g., naturally occurring allelic variants) to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. In other embodiments, the invention provides a nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3, wherein the nucleic acid encodes a full length 57242 protein or an active fragment thereof.

[0009] In a related aspect, the invention further provides nucleic acid constructs which include a 57242 nucleic acid molecule described herein. In certain embodiments, the nucleic acid molecules of the invention are operatively linked to native or heterologous regulatory sequences. Also included, are vectors and host cells containing the 57242 nucleic acid molecules of the invention e.g., vectors and host cells suitable for producing 57242 nucleic acid molecules and polypeptides.

[0010] In another related aspect, the invention provides nucleic acid fragments suitable as primers or hybridization probes for the detection of 57242-encoding nucleic acids.

[0011] In still another related aspect, isolated nucleic acid molecules that are antisense to a 57242 encoding nucleic acid molecule are provided.

[0012] In another aspect, the invention features, 57242 polypeptides, and biologically active or antigenic fragments thereof that are useful, e.g., as reagents or targets in assays applicable to treatment and diagnosis of 57242-mediated or -related disorders. In another embodiment, the invention provides 57242 polypeptides having a 57242 activity. Preferred polypeptides are 57242 proteins including at least one G protein-coupled receptor domain, and, preferably, having a 57242 activity, e.g., a 57242 activity as described herein.

[0013] In other embodiments, the invention provides 57242 polypeptides, e.g., a 57242 polypeptide having the amino acid sequence shown in SEQ ID NO:2; an amino acid sequence that is substantially identical to the amino acid sequence shown in SEQ ID NO:2; or an amino acid sequence encoded by a nucleic acid molecule having a nucleotide sequence which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3, wherein the nucleic acid encodes a full length 57242 protein or an active fragment thereof.

[0014] In a related aspect, the invention further provides nucleic acid constructs which include a 57242 nucleic acid molecule described herein.

[0015] In a related aspect, the invention provides 57242 polypeptides or fragments operatively linked to non-57242 polypeptides to form fusion proteins.

[0016] In another aspect, the invention features antibodies and antigen-binding fragments thereof, that react with, or more preferably specifically bind 57242 polypeptides.

[0017] The present invention is based, at least in part, on the discovery that 57242 molecules are expressed at increased levels in adipose tissue, *e.g.*, white adipose tissue (WAT) and brown adipose tissue (BAT) (see Examples 1-3 and Tables 2-8 described herein). 57242 molecules were further found to be upregulated during adipocyte differentiation, and downregulated during exposure to cold, cAMP, or starvation conditions (*i.e.*, under conditions that affect brown or white adipocyte metabolism) (see Example 3 and Tables 3-6, 8), as well as in genetic models of obesity (see Example 3 and Table 7).

[0018] Accordingly, the present invention provides methods for the diagnosis and treatment of metabolic disorders including but not limited to obesity, anorexia, cachexia, hyperlipidemia and diabetes.

[0019] In one aspect, the invention provides methods of screening for compounds that modulate the expression or activity of the 57242 polypeptides or nucleic acids. The method includes contacting a sample expressing a 57242 nucleic acid or polypeptide with a test compound and assaying the ability of the test compound to modulate the expression of a 57242 nucleic acid or the activity of a 57242 polypeptide.

[0020] In one embodiment, the invention provides methods for identifying a compound capable of treating a metabolic disorder, *e.g.*, obesity, anorexia, cachexia, hyperlipidemia, and diabetes. The method includes assaying the ability of the compound to modulate 57242 nucleic acid expression or 57242 polypeptide activity. In one embodiment, the ability of the compound to modulate nucleic acid expression or 57242 polypeptide activity is determined by detecting modulation of lipogenesis. In another embodiment, the ability of the compound to modulate nucleic acid expression or 57242 polypeptide activity is determined by detecting modulation of lipolysis. In still another embodiment, the ability of the compound to modulate nucleic acid expression or 57242 polypeptide activity is determined by detecting modulation of hyperplastic growth. In yet another embodiment, the ability of the compound to modulate nucleic acid expression or 57242 polypeptide activity is determined by detecting modulation of hypertrophic growth.

[0021] In another aspect, the invention provides methods for identifying a compound capable of modulating an adipocyte activity, *e.g.*, hyperplastic growth, hypertrophic growth, or lipogenesis. The method includes contacting an adipocyte expressing a 57242 nucleic acid or polypeptide with a test compound and assaying the ability of the test compound to modulate the expression of a 57242 nucleic acid or the activity of a 57242 polypeptide.

[0022] In another aspect, the invention provides methods for modulating an adipocyte activity, *e.g.*, hyperplastic growth, hypertrophic growth, or lipogenesis. The method includes contacting an adipocyte with a 57242 modulator, for example, an anti-57242 antibody, a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2 or a fragment thereof, a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, a small molecule, an antisense 57242 nucleic acid molecule, a nucleic acid molecule of SEQ ID NO:1 or a fragment thereof, or a ribozyme.

[0023] In still another aspect, the invention provides a process for modulating 57242 polypeptide or nucleic acid expression or activity, *e.g.* using the screened compounds. In certain embodiments, the methods involve treatment of conditions related to aberrant activity or expression of the 57242 polypeptides or nucleic acids, such as conditions involving aberrant or deficient cellular proliferation or differentiation.

[0024] The invention also provides assays for determining the activity of or the presence or absence of 57242 polypeptides or nucleic acid molecules in a biological sample, including for disease diagnosis. In one aspect, provided are assays for determining the presence or absence of a genetic alteration in a 57242 polypeptide or nucleic acid molecule, including for disease diagnosis.

[0025] In one embodiment, methods include identifying a nucleic acid associated with a metabolic disorder, *e.g.*, obesity, anorexia, cachexia, hyperlipidemia, and diabetes.

[0026] In yet another aspect, the invention features a method for identifying a subject having a metabolic disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression, *e.g.*, obesity, anorexia, or cachexia. The method includes contacting a sample obtained from the subject and expressing a 57242 nucleic acid or polypeptide with a test compound and assaying the ability of the test compound to modulate the expression of a 57242 nucleic acid or the activity of a 57242 polypeptide.

[0027] In yet another aspect, the invention features a method for treating a subject having a metabolic disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression, *e.g.*, obesity, diabetes, hyperlipidemia, anorexia, or cachexia. The method includes administering to the subject a 57242 modulator, *e.g.*, in a pharmaceutically acceptable formulation or by using a gene therapy vector. Embodiments of this aspect of the invention include the 57242 modulator being any of a small molecule, an anti-57242 antibody, a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2 or a fragment thereof, a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2, an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, an antisense 57242 nucleic acid molecule, a nucleic acid molecule of SEQ ID NO:1 or a fragment thereof, or a ribozyme.

[0028] Other features and advantages of the invention will be apparent from the following detailed description and claims.

#### Detailed Description

[0029] Here we describe a novel GPCR, 57242, which is highly and specifically expressed in human and mouse adipocytes and which expression is regulated under conditions that change adipocyte metabolism both *in vitro* and *in vivo*. 57242 is therefore a candidate target to identify small molecules for the treatment of diabetes, obesity and/or lipid disorders in humans.

#### Human 57242

[0030] The human 57242 sequence (SEQ ID NO:1), which is approximately 1194 nucleotides long including untranslated regions, contains a predicted methionine-initiated coding sequence of about 1041 nucleotides (nucleotides 154-1194 of SEQ ID NO:1; SEQ ID NO:3), not including the terminal codon. The coding sequence encodes a 346 amino acid protein (SEQ ID NO:2).

[0031] In one embodiment, a 57242 molecule may include a signal sequence. As used herein, a "signal sequence" refers to a peptide of about 10-80 amino acid residues in length which occurs at the N-terminus of secretory and integral membrane proteins and which contains a majority of hydrophobic amino acid residues. For example, a signal sequence contains at least about 20-60 amino acid residues, preferably about 30-50 amino acid

residues, more preferably about 37 amino acid residues, and has at least about 40-70%, preferably about 50-65%, and more preferably about 55-60% hydrophobic amino acid residues (e.g., alanine, valine, leucine, isoleucine, phenylalanine, tyrosine, tryptophan, or proline). Such a "signal sequence", also referred to in the art as a "signal peptide", serves to direct a protein containing such a sequence to a lipid bilayer. For example, in one embodiment, a 57242 protein contains a signal sequence of about amino acids 1-37 of SEQ ID NO:2. The "signal sequence" is cleaved during processing of the mature protein. In this embodiment, the mature 57242 protein corresponds to amino acids 38-346 of SEQ ID NO:2.

**[0032]** Therefore, the mature protein form is approximately 346 amino acid residues in length (from about amino acid 1 to amino acid 346 of SEQ ID NO:2) or, if a signal sequence is present, from about 309 amino acids in length (from about amino acid 37 to amino acid 346 of SEQ ID NO:2). Human 57242 contains the following regions or other structural features: a predicted G protein-coupled receptor domain located at about amino acid residues 32-278 of SEQ ID NO:2; and predicted transmembrane domains which extend from about amino acid residue 21-42, 52-70, 90-111, 131-152, 185-201, 221-245, and 259-280 of SEQ ID NO:2; or if a signal sequence is present, predicted transmembrane domains extend from about amino acid residue 53-71, 91-112, 132-153, 186-202, 222-246, and 260-281 of SEQ ID NO:2.

**[0033]** The mature human 57242 protein contains the following structural features: a predicted seven transmembrane (7TM) domain located at about amino acids 32-278 of SEQ ID NO:2. The seven transmembrane domain shows homology to members of the rhodopsin family. In one embodiment, predicted transmembrane domains extend from about amino acid 21 (extracellular end) to about amino acid 42 (cytoplasmic end) of SEQ ID NO:2; from about amino acid 52 (cytoplasmic end) to about amino acid 70 (extracellular end) of SEQ ID NO:2; from about amino acid 90 (extracellular end) to about amino acid 111 (cytoplasmic end) of SEQ ID NO:2; from about amino acid 131 (cytoplasmic end) to about amino acid 152 (extracellular end) of SEQ ID NO:2; from about amino acid 185 (extracellular end) to about amino acid 201 (cytoplasmic end) of SEQ ID NO:2; from about amino acid 221 (cytoplasmic end) to about amino acid 245 (extracellular end) of SEQ ID NO:2; and from about amino acid 259 (extracellular end) to about amino acid 280 (cytoplasmic end); three cytoplasmic loops found at about amino acids 43-51, 112-130, and 202-220 of SEQ ID NO:2; three extracellular loops found at about amino acid 71-89, 153-184, and 245-258 of SEQ ID NO:2; and a C-terminal cytoplasmic domain is found at about amino acid residues

281-346 of SEQ ID NO:2. Predicted transmembrane domains may be identified by ORF analysis with MEMSAT.

**[0034]** In another embodiment, predicted transmembrane domains extend from about amino acid 53 (cytoplasmic end) to about amino acid 71 (extracellular end) of SEQ ID NO:2; from about amino acid 91 (extracellular end) to about amino acid 112 (cytoplasmic end) of SEQ ID NO:2; from about amino acid 132 (cytoplasmic end) to about amino acid 153 (extracellular end) of SEQ ID NO:2; from about amino acid 186 (extracellular end) to about amino acid 202 (cytoplasmic end) of SEQ ID NO:2; from about amino acid 222 (cytoplasmic end) to about amino acid 246 (extracellular end) of SEQ ID NO:2; and from about amino acid 260 (extracellular end) to about amino acid 281 (cytoplasmic end); two cytoplasmic loops found at about amino acids 113-131 and 203-221, of SEQ ID NO:2; three extracellular loops found at about amino acid 72-90, 154-185, and 247-259 of SEQ ID NO:2; and a C-terminal cytoplasmic domain is found at about amino acid residues 282-346 of SEQ ID NO:2.

**[0035]** The 57242 protein also includes the following domains: one N-glycosylation site (PS00001) located at about amino acids 3-6 of SEQ ID NO:2; one cAMP- and cGMP-dependent protein kinase phosphorylation site (PS00004) located at about amino acids 216-219 of SEQ ID NO:2; seven predicted protein kinase C phosphorylation sites (PS00005) located at about amino acids 46-48, 128-130, 196-198, 202-204, 238-240, 296-298, and 307-309 of SEQ ID NO:2; three predicted casein kinase II phosphorylation sites (PS00006) located at about amino 250-253, 271-274, and 332-335 of SEQ ID NO:2; two predicted N-myristoylation sites (PS00008) located at about amino acids 29-34 and 134-139 of SEQ ID NO:2; one predicted amidation site (PS00009) located at about amino acids 318-321 of SEQ ID NO:2; and one G-protein coupled receptors signature site (PS00237) located at about amino acids 101-117 of SEQ ID NO:2.

Based on 57242 protein sequence, cellular localization signals can be identified by methods known to one of skill in the art (e.g., PSORT Prediction). Table 1 depicts predicted subcellular localization of 57242, generated using PSORT Prediction software.

**TABLE 1 Subcellular Localization of 57242**

<b>MITDISC: discrimination of mitochondrial targeting seq</b>
R content: 1 Hyd Moment(75): 11.18
Hyd Moment(95): 5.39 G content: 2
D/E content: 2 S/T content: 1
Score: -6.17
<b>Gavel: prediction of cleavage sites for mitochondrial preseq</b>
R-2 motif at 18 CR <sup>1</sup> EG
<b>NUCDISC: discrimination of nuclear localization signals</b>
pat4: RRRH (3) at 77 pat7: none
bipartite: RRRQQLARQARMKKATR at 204
content of basic residues: 9.0%
NLS Score: 0.21
<b>Final Results (k = 9/23):</b>
55.6 %: endoplasmic reticulum
22.2 %: vacuolar
11.1 %: Golgi
11.1 %: mitochondrial
prediction for 57242 is end (k=9)

[0036] For general information regarding PSORT, Prosite and PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer et al. (1997) *Protein* 28:405-420 and <http://www.psc.edu/general/software/packages/pfam/pfam.html>.

[0037] The 57242 protein contains a significant number of structural characteristics in common with members of the G protein-coupled receptor family. The term "family" when referring to the protein and nucleic acid molecules of the invention means two or more proteins or nucleic acid molecules having a common structural domain or motif and having sufficient amino acid or nucleotide sequence homology as defined herein. Such family members can be naturally or non-naturally occurring and can be from either the same or different species. For example, a family can contain a first protein of human origin as well as other distinct proteins of human origin, or alternatively, can contain homologues of non-human origin, e.g., rat or mouse proteins. Members of a family can also have common functional characteristics.

[0038] As used herein, the term "G protein-coupled receptor" or "GPCR" refers to a family of proteins that preferably comprise an N-terminal extracellular domain, seven transmembrane domains (also referred to as membrane-spanning domains), three extracellular domains (also referred to as extracellular loops), three cytoplasmic domains (also referred to as cytoplasmic loops), and a C-terminal cytoplasmic domain (also referred to as a cytoplasmic tail). Members of the GPCR family also share certain conserved amino acid residues, some of which have been determined to be critical to receptor function and/or G protein signaling. For example, GPCRs usually contain the following features including a conserved asparagine residue in the first transmembrane domain. An alignment of the transmembrane domains of representative GPCRs can be found at <http://mgdkk1.nidll.nih.gov:8000/extended.html>.

[0039] Based on structural similarities, members of the GPCR family have been classified into various subfamilies, including: Subfamily I which comprises receptors typified by rhodopsin and the beta2-adrenergic receptor and currently contains over 200 unique members (reviewed by Dohlman *et al.* (1991) *Annu. Rev. Biochem.* 60:653-688); Subfamily II, which includes the parathyroid hormone/calcitonin/secretin receptor family (Juppner *et al.* (1991) *Science* 254:1024-1026; Lin *et al.* (1991) *Science* 254:1022-1024); Subfamily III, which includes the metabotropic glutamate receptor family in mammals, such as the GABA receptors (Nakanishi *et al.* (1992) *Science* 258: 597-603); Subfamily IV, which includes the cAMP receptor family that is known to mediate the chemotaxis and development of *D. discoideum* (Klein *et al.* (1988) *Science* 241:1467-1472); and Subfamily V, which includes the fungal mating pheromone receptors such as STE2 (reviewed by Kurjan I *et al.* (1992) *Annu. Rev. Biochem.* 61:1097-1129). Within each family, distinct, highly conserved motifs have been identified. These motifs have been suggested to be critical for the structural integrity of the receptor, as well as for coupling to G proteins.

[0040] Based on the results from the HMM analysis (HMMER Version 2.1.1), the 57242 polypeptide appears to belong to the rhodopsin subfamily of GPCRs (family 1).

[0041] In one embodiment, a 57242 protein includes at least one "7 transmembrane receptor profile" or regions homologous with a "7 transmembrane receptor profile". As used herein, the term "7 transmembrane receptor profile" includes an amino acid sequence having at least about 50-400, preferably about 150-300, more preferably about 200-275 amino acid residues, or at least about 246 amino acids in length and having a bit score for the alignment of the sequence to the 7tm\_1 family Hidden Markov Model (HMM) of at least

10, preferably 20-30, more preferably 22-40, more preferably 40-50, 50-75, 75-100, 100-200 or greater.

[0042] To identify the presence of a 7 transmembrane receptor profile in a 57242 receptor, the amino acid sequence of the protein is searched against a database of HMMs (e.g., the Pfam database, release 2.1) using the default parameters ([http://www.sanger.ac.uk/Software/Pfam/HMM\\_search](http://www.sanger.ac.uk/Software/Pfam/HMM_search)). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for PF00001 and score of 15 is the default threshold score for determining a hit. Alternatively, the seven transmembrane domain can be predicted based on stretches of hydrophobic amino acids forming  $\square$ -helices (SOUSI server). For example, using a SOUSI server, a 7 TM receptor profile was identified in the amino acid sequence of SEQ ID NO:2 (e.g., amino acids 32-278 of SEQ ID NO:2). Accordingly, 57242 proteins having at least 50-60% homology, preferably about 60-70%, more preferably about 70-80%, or about 80-90% homology with the 7 transmembrane receptor profile of human 57242 are within the scope of the invention.

[0043] In one embodiment, a 57242 protein includes at least one transmembrane domain. As used herein, the term "transmembrane domain" includes an amino acid sequence of about 15 amino acid residues in length that spans a phospholipid membrane. More preferably, a transmembrane domain includes about at least 16, 17, 18, 20, 21, 22, 23, or 24 amino acid residues and spans a phospholipid membrane. Transmembrane domains are rich in hydrophobic residues, and typically have an  $\alpha$ -helical structure. In a preferred embodiment, at least 50%, 60%, 70%, 80%, 90%, 95% or more of the amino acids of a transmembrane domain are hydrophobic, e.g., leucines, isoleucines, tyrosines, or tryptophans. Transmembrane domains are described in, for example, <http://pfam.wustl.edu/cgi-bin/getdesc?name=7tm-1>, and Zagotta W.N. et al., (1996) *Annual Rev. Neurosci.* 19: 235-63, the contents of which are incorporated herein by reference.

[0044] In a preferred embodiment, a 57242 polypeptide or protein has at least one transmembrane domain or a region which includes at least 16, 17, 18, 20, 21, 22, 23, or 24 amino acid residues and has at least about 60%, 70% 80% 90% 95%, 99%, or 100% homology with a "transmembrane domain," e.g., at least one transmembrane domain of human 57242 (e.g., amino acid residues 21-42, 52-70, 90-111, 131-152, 185-201, 221-245, and 259-280 of SEQ ID NO:2).

**[0045]** In another embodiment, a 57242 protein includes at least one “non-transmembrane domain.” As used herein, “non-transmembrane domains” are domains that reside outside of the membrane. When referring to plasma membranes, non-transmembrane domains include extracellular domains (i.e., outside of the cell) and intracellular domains (i.e., within the cell). When referring to membrane-bound proteins found in intracellular organelles (e.g., mitochondria, endoplasmic reticulum, peroxisomes and microsomes), non-transmembrane domains include those domains of the protein that reside in the cytosol (i.e., the cytoplasm), the lumen of the organelle, or the matrix or the intermembrane space (the latter two relate specifically to mitochondria organelles). The C-terminal amino acid residue of a non-transmembrane domain is adjacent to an N-terminal amino acid residue of a transmembrane domain in a naturally-occurring 57242, or 57242-like protein.

**[0046]** In a preferred embodiment, a 57242 polypeptide or protein has a “non-transmembrane domain” or a region which includes at least about 1-100, preferably about 2-80, more preferably about 5-70, and even more preferably about 8-65 amino acid residues, and has at least about 60%, 70% 80% 90% 95%, 99% or 100% homology with a “non-transmembrane domain”, e.g., a non-transmembrane domain of human 57242 (e.g., residues 1-20, 43-51, 71-89, 112-130, 153-184, 202-220, 246-255, and 281-346 of SEQ ID NO:2). Preferably, a non-transmembrane domain is capable of catalytic activity.

**[0047]** In another embodiment, a 57242 protein include at least one extracellular loop. As defined herein, the term “loop” includes an amino acid sequence having a length of at least about 5, preferably about 6-10, and more preferably about 12-31 amino acid residues, and has an amino acid sequence that connects two transmembrane domains within a protein or polypeptide. Accordingly, the N-terminal amino acid of a loop is adjacent to a C-terminal amino acid of a transmembrane domain in a naturally-occurring a 57242, or a 57242-like molecule, and the C-terminal amino acid of a loop is adjacent to an N-terminal amino acid of a transmembrane domain in a naturally-occurring 57242, or a 57242-like molecule. As used herein, an “extracellular loop” includes an amino acid sequence located outside of a cell, or extracellularly. For example, extracellular loops can be found at about amino acids 71-89, 153-184, and 246-258 of SEQ ID NO:2.

**[0048]** In a preferred embodiment, a 57242 polypeptide or protein has at least one extracellular loop or a region which includes at least about 4, preferably about 5-10, preferably about 10-20, and more preferably about 12-31 amino acid residues and has at least about 60%, 70% 80% 90% 95%, 99%, or 100% homology with an “extracellular loop.”

*e.g.*, at least one extracellular loop of human 57242 (*e.g.*, residues 71-89, 153-184, and 246-258 of SEQ ID NO:2).

[0049] In another embodiment, a 57242 protein includes at least one cytoplasmic loop, also referred to herein as a cytoplasmic domain. As used herein, a "cytoplasmic loop" includes an amino acid sequence having a length of at least about 4, preferably about 5-7, and more preferably about 8-18 amino acid residues located within a cell or within the cytoplasm of a cell. For example, a cytoplasmic loop is found at about amino acids 43-51, 112-130, and 202-220 of SEQ ID NO:2.

[0050] In a preferred embodiment, a 57242 polypeptide or protein has at least one cytoplasmic loop or a region which includes at least about 5, preferably about 5-10, and more preferably about 10-20 amino acid residues and has at least about 60%, 70% 80% 90% 95%, 99%, or 100% homology with an "cytoplasmic loop," *e.g.*, at least one cytoplasmic loop of human 57242 (*e.g.*, residues 43-51, 112-130, and 202-220 of SEQ ID NO:2).

[0051] A non-transmembrane domain located at the N-terminus of a 57242 protein or polypeptide is referred to herein as an "N-terminal non-transmembrane domain." As used herein, an "N-terminal non-transmembrane domain" includes an amino acid sequence having about 1-50, preferably about 5-30, more preferably about 10-25, or even more preferably about 20 amino acid residues in length and is located outside the boundaries of a membrane. For example, an N-terminal non-transmembrane domain is located at about amino acid residues 1-20 of SEQ ID NO:2.

[0052] Similarly, a non-transmembrane domain located at the C-terminus of a 57242 protein or polypeptide is referred to herein as a "C-terminal non-transmembrane domain." As used herein, a "C-terminal non-transmembrane domain" includes an amino acid sequence having about 10-100, preferably about 30-80, preferably about 55-75, more preferably about 65 amino acid residues in length and is located outside the boundaries of a membrane. For example, a C-terminal non-transmembrane domain is located at about amino acid residues 281-346 of SEQ ID NO:2.

[0053] As the 57242 polypeptides of the invention may modulate 57242-mediated activities, they may be useful for developing novel diagnostic and therapeutic agents for 57242-mediated or related disorders, as described below.

[0054] As used herein, a "57242 activity", "biological activity of 57242" or "functional activity of 57242", refers to an activity exerted by a 57242 protein, polypeptide or nucleic acid molecule on *e.g.*, a 57242-responsive cell or on a 57242 substrate, *e.g.*, a protein

substrate, as determined *in vivo* or *in vitro*. In one embodiment, a 57242 activity is a direct activity, such as an association with a 57242 target molecule. A “target molecule” or “binding partner” is a molecule with which a 57242 protein binds or interacts in nature. In an exemplary embodiment, is a 57242 receptor. A 57242 activity can also be an indirect activity, *e.g.*, a cellular signalling activity mediated by interaction of the 57242 protein with a 57242 receptor.

[0055] The 57242 molecules of the present invention are predicted to have similar biological activities as G-protein coupled receptor family members. For example, the 57242 proteins of the present invention can have one or more of the following activities: (1) regulating, sensing and/or transmitting an extracellular signal into a cell, (for example, a fat cell (*e.g.*, an adipocyte), a bone cell (*e.g.*, an osteoclast or an osteoblast), a hematopoietic cell, a neural cell); (2) interacting with (*e.g.*, binding to) an extracellular signal or a cell surface receptor; (3) mobilizing an intracellular molecule that participates in a signal transduction pathway (*e.g.*, adenylate cyclase or phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>), inositol 1,4,5-triphosphate (IP<sub>3</sub>)); (4) regulating polarization of the plasma membrane; (5) controlling production or secretion of molecules; (6) altering the structure of a cellular component; (7) modulating cell proliferation, *e.g.*, synthesis of DNA; and (8) modulating cell migration, cell differentiation; and cell survival. Thus, the 57242 molecules can act as novel diagnostic targets and therapeutic agents for controlling G-protein coupled receptor-related disorders. Other activities, as described below, include the ability to modulate function, survival, morphology, proliferation and/or differentiation of cells of tissues in which 57242 molecules are expressed (*e.g.*, adipocytes).

[0056] The response mediated by a 57242 receptor protein depends on the type of cell. For example, in some cells, binding of a ligand to the receptor protein may stimulate an activity such as release of compounds, gating of a channel, cellular adhesion, migration, differentiation, etc., through phosphatidylinositol or cyclic AMP metabolism and turnover while in other cells, the binding of the ligand will produce a different result. Regardless of the cellular activity/response modulated by the receptor protein, it is universal that the protein is a GPCR and interacts with G proteins to produce one or more secondary signals, in a variety of intracellular signal transduction pathways, *e.g.*, through phosphatidylinositol or cyclic AMP metabolism and turnover, in a cell. As used herein, a “signaling transduction pathway” refers to the modulation (*e.g.*, stimulation or inhibition) of a cellular function/activity upon the binding of a ligand to the GPCR (57242 protein). Examples of such functions include

mobilization of intracellular molecules that participate in a signal transduction pathway, *e.g.*, phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>), inositol 1,4,5-triphosphate (IP<sub>3</sub>) and adenylate cyclase.

[0057] As used herein, "phosphatidylinositol turnover and metabolism" refers to the molecules involved in the turnover and metabolism of phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>) as well as to the activities of these molecules. PIP<sub>2</sub> is a phospholipid found in the cytosolic leaflet of the plasma membrane. Binding of ligand to the receptor activates, in some cells, the plasma-membrane enzyme phospholipase C that in turn can hydrolyze PIP<sub>2</sub> to produce 1,2-diacylglycerol (DAG) and inositol 1,4,5-triphosphate (IP<sub>3</sub>). Once formed IP<sub>3</sub> can diffuse to the endoplasmic reticulum surface where it can bind an IP<sub>3</sub> receptor, *e.g.*, a calcium channel protein containing an IP<sub>3</sub> binding site. IP<sub>3</sub> binding can induce opening of the channel, allowing calcium ions to be released into the cytoplasm. IP<sub>3</sub> can also be phosphorylated by a specific kinase to form inositol 1,3,4,5-tetraphosphate (IP<sub>4</sub>), a molecule which can cause calcium entry into the cytoplasm from the extracellular medium. IP<sub>3</sub> and IP<sub>4</sub> can subsequently be hydrolyzed very rapidly to the inactive products inositol 1,4-bisphosphate (IP<sub>2</sub>) and inositol 1,3,4-triphosphate, respectively. These inactive products can be recycled by the cell to synthesize PIP<sub>2</sub>. The other second messenger produced by the hydrolysis of PIP<sub>2</sub>, namely 1,2-diacylglycerol (DAG), remains in the cell membrane where it can serve to activate the enzyme protein kinase C. Protein kinase C is usually found soluble in the cytoplasm of the cell, but upon an increase in the intracellular calcium concentration, this enzyme can move to the plasma membrane where it can be activated by DAG. The activation of protein kinase C in different cells results in various cellular responses such as the phosphorylation of glycogen synthase, or the phosphorylation of various transcription factors, *e.g.*, NF- $\kappa$ B. The language "phosphatidylinositol activity", as used herein, refers to an activity of PIP<sub>2</sub> or one of its metabolites.

[0058] Another signaling pathway in which the receptor may participate is the cAMP turnover pathway. As used herein, "cyclic AMP turnover and metabolism" refers to the molecules involved in the turnover and metabolism of cyclic AMP (cAMP) as well as to the activities of these molecules. Cyclic AMP is a second messenger produced in response to ligand-induced stimulation of certain G protein coupled receptors. In the cAMP signaling pathway, binding of a ligand to a GPCR can lead to the activation of the enzyme adenylyl cyclase, which catalyzes the synthesis of cAMP. The newly synthesized cAMP can in turn activate a cAMP-dependent protein kinase. This activated kinase can phosphorylate a

voltage-gated potassium channel protein, or an associated protein, and lead to the inability of the potassium channel to open during an action potential. The inability of the potassium channel to open results in a decrease in the outward flow of potassium, which normally repolarizes the membrane of a neuron, leading to prolonged membrane depolarization.

[0059] Based on the above-described sequence similarities, the 57242 molecules of the present invention are predicted to have similar biological activities as G-protein coupled receptor family members. Thus, the 57242 molecules can act as novel diagnostic targets and therapeutic agents for controlling one or more of cellular proliferative and/or differentiative disorders, disorders associated with adipocyte differentiation and metabolism and metabolic disorders, as well as bone metabolism, hematopoietic disorders, cardiovascular disorders, liver disorders, viral diseases, pain or immune disorders.

[0060] The present invention is based, at least in part, on the discovery that the 57242 nucleic acid and polypeptide molecules are expressed at high levels in adipose tissue, are regulated during conditions which affect differentiation and metabolism of adipocytes, and are downregulated in genetic animal models of obesity (see Examples and Tables described herein). Without intending to be limited by mechanism, it is believed that 57242 molecules can modulate the metabolism by (directly or indirectly) affecting the rate of lipogenesis and/or lipolysis.

[0061] As used herein, the term "metabolic disorder" includes a disorder, disease or condition which is caused or characterized by an abnormal metabolism (*i.e.*, the chemical changes in living cells by which energy is provided for vital processes and activities) in a subject. Metabolic disorders include diseases, disorders, or conditions associated with aberrant thermogenesis or aberrant adipose cell (*e.g.*, brown or white adipose cell) content or function. Metabolic disorders can be characterized by a misregulation (*e.g.*, downregulation or upregulation) of 57242 activity. Metabolic disorders can detrimentally affect cellular functions such as cellular proliferation, growth, differentiation, or migration, cellular regulation of homeostasis, inter- or intra-cellular communication; tissue function, such as liver function, muscle function, or adipocyte function; systemic responses in an organism, such as hormonal responses (*e.g.*, insulin response). Examples of metabolic disorders include obesity, diabetes, hyperphagia, endocrine abnormalities, triglyceride storage disease, Bardet-Biedl syndrome, Lawrence-Moon syndrome, Prader-Labhart-Willi syndrome, anorexia, and cachexia. Obesity is defined as a body mass index (BMI) of  $30 \text{ kg/m}^2$  or more (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and

Treatment of Overweight and Obesity in Adults (1998)). However, the present invention is also intended to include a disease, disorder, or condition that is characterized by a body mass index (BMI) of 25 kg<sup>2</sup>/m or more, 26 kg<sup>2</sup>/m or more, 27 kg<sup>2</sup>/m or more, 28 kg<sup>2</sup>/m or more, 29 kg<sup>2</sup>/m or more, 29.5 kg<sup>2</sup>/m or more, or 29.9 kg<sup>2</sup>/m or more, all of which are typically referred to as overweight (National Institute of Health, Clinical Guidelines on the Identification, Evaluation, and Treatment of Overweight and Obesity in Adults (1998)).

**[0062]** As used interchangeably herein, "57242 activity," "biological activity of 57242" or "functional activity of 57242," includes an activity exerted by a 57242 protein, polypeptide or nucleic acid molecule on a 57242 responsive cell or tissue, *e.g.*, adipocytes, or on a 57242 protein substrate, as determined *in vivo*, or *in vitro*, according to standard techniques. 57242-mediated function can include modulation of metabolism. Examples of such target molecules include proteins in the same signaling path as the 57242 protein, *e.g.*, proteins which may function upstream (including both stimulators and inhibitors of activity) or downstream of the 57242 protein in a pathway involving regulation of metabolism. The biological activities of 57242 proteins can have one or more of the following activities: 1) modulation of fat homeostasis; 2) modulation of lipogenesis (*e.g.*, fat deposition necessary for heat insulation, mechanical cushion, and/or storage); 3) modulation of lipolysis (*e.g.*, fat mobilization necessary as an energy source and/or for thermogenesis); and 4) modulation of adipocyte growth (*e.g.*, hyperplastic and/or hypertrophic growth).

**[0063]** As used herein, "metabolic activity" includes an activity exerted by an adipose cell, or an activity that takes place in an adipose cell. For example, such activities include cellular processes that contribute to the physiological role of adipose cells, such as lipogenesis and lipolysis and include, but are not limited to, cell proliferation, differentiation, growth, migration, programmed cell death, uncoupled mitochondrial respiration, and thermogenesis.

**[0064]** Examples of cellular proliferative and/or differentiative disorders include cancer, *e.g.*, carcinoma, sarcoma, metastatic disorders or hematopoietic neoplastic disorders, *e.g.*, leukemias. A metastatic tumor can arise from a multitude of primary tumor types, including but not limited to those of prostate, colon, lung, breast and liver origin.

**[0065]** As used herein, the terms "cancer", "hyperproliferative" and "neoplastic" refer to cells having the capacity for autonomous growth, *i.e.*, an abnormal state or condition characterized by rapidly proliferating cell growth. Hyperproliferative and neoplastic disease states may be categorized as pathologic, *i.e.*, characterizing or constituting a disease state, or

may be categorized as non-pathologic, i.e., a deviation from normal but not associated with a disease state. The term is meant to include all types of cancerous growths or oncogenic processes, metastatic tissues or malignantly transformed cells, tissues, or organs, irrespective of histopathologic type or stage of invasiveness. "Pathologic hyperproliferative" cells occur in disease states characterized by malignant tumor growth. Examples of non-pathologic hyperproliferative cells include proliferation of cells associated with wound repair.

[0066] The terms "cancer" or "neoplasms" include malignancies of the various organ systems, such as affecting lung, breast, thyroid, lymphoid, gastrointestinal, and genito-urinary tract, as well as adenocarcinomas which include malignancies such as most colon cancers, renal-cell carcinoma, prostate cancer and/or testicular tumors, non-small cell carcinoma of the lung, cancer of the small intestine and cancer of the esophagus.

[0067] The term "carcinoma" is art recognized and refers to malignancies of epithelial or endocrine tissues including respiratory system carcinomas, gastrointestinal system carcinomas, genitourinary system carcinomas, testicular carcinomas, breast carcinomas, prostatic carcinomas, endocrine system carcinomas, and melanomas. Exemplary carcinomas include those forming from tissue of the cervix, lung, prostate, breast, head and neck, colon and ovary. The term also includes carcinosarcomas, e.g., which include malignant tumors composed of carcinomatous and sarcomatous tissues. An "adenocarcinoma" refers to a carcinoma derived from glandular tissue or in which the tumor cells form recognizable glandular structures.

[0068] The term "sarcoma" is art recognized and refers to malignant tumors of mesenchymal derivation.

[0069] The 57242 nucleic acid and protein of the invention can be used to treat and/or diagnose a variety of proliferative disorders. E.g., such disorders include hematopoietic neoplastic disorders. As used herein, the term "hematopoietic neoplastic disorders" includes diseases involving hyperplastic/neoplastic cells of hematopoietic origin, e.g., arising from myeloid, lymphoid or erythroid lineages, or precursor cells thereof. Preferably, the diseases arise from poorly differentiated acute leukemias, e.g., erythroblastic leukemia and acute megakaryoblastic leukemia. Additional exemplary myeloid disorders include, but are not limited to, acute promyeloid leukemia (APML), acute myelogenous leukemia (AML) and chronic myelogenous leukemia (CML) (reviewed in Vaickus, L., (1991) *Crit. Rev. in Oncol./Hematol.* 11:267-97); lymphoid malignancies include, but are not limited to acute lymphoblastic leukemia (ALL) which includes B-lineage ALL and T-lineage ALL, chronic

lymphocytic leukemia (CLL), prolymphocytic leukemia (PLL), hairy cell leukemia (HLL) and Waldenstrom's macroglobulinemia (WM). Additional forms of malignant lymphomas include, but are not limited to non-Hodgkin lymphoma and variants thereof, peripheral T cell lymphomas, adult T cell leukemia/lymphoma (ATL), cutaneous T-cell lymphoma (CTCL), large granular lymphocytic leukemia (LGF), Hodgkin's disease and Reed-Sternberg disease.

[0070] The 57242 protein, fragments thereof, and derivatives and other variants of the sequence in SEQ ID NO:2 are collectively referred to as "polypeptides or proteins of the invention" or "57242 polypeptides or proteins". Nucleic acid molecules encoding such polypeptides or proteins are collectively referred to as "nucleic acids of the invention" or "57242 nucleic acids." 57242 molecules refer to 57242 nucleic acids, polypeptides, and antibodies.

[0071] As used herein, the term "nucleic acid molecule" includes DNA molecules (e.g., a cDNA or genomic DNA) and RNA molecules (e.g., an mRNA) and analogs of the DNA or RNA generated, e.g., by the use of nucleotide analogs. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA.

[0072] The term "isolated or purified nucleic acid molecule" includes nucleic acid molecules which are separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. For example, with regards to genomic DNA, the term "isolated" includes nucleic acid molecules which are separated from the chromosome with which the genomic DNA is naturally associated. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (i.e., sequences located at the 5' and/or 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of 5' and/or 3' nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular material, or culture medium when produced by recombinant techniques, or substantially free of chemical precursors or other chemicals when chemically synthesized.

[0073] As used herein, the term "hybridizes under stringent conditions" describes conditions for hybridization and washing. Stringent conditions are known to those skilled in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons,

N.Y. (1989), 6.3.1-6.3.6. Aqueous and nonaqueous methods are described in that reference and either can be used. A preferred example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50°C. Another example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 55°C. A further example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 60°C. Preferably, stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 65°C. Particularly preferred stringency conditions (and the conditions that should be used if the practitioner is uncertain about what conditions should be applied to determine if a molecule is within a hybridization limitation of the invention) are 0.5M Sodium Phosphate, 7% SDS at 65°C, followed by one or more washes at 0.2X SSC, 1% SDS at 65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of SEQ ID NO:1, or SEQ ID NO:3, corresponds to a naturally-occurring nucleic acid molecule.

[0074] As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

[0075] As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules which include an open reading frame encoding a 57242 protein, preferably a mammalian 57242 protein, and can further include non-coding regulatory sequences, and introns.

[0076] An "isolated" or "purified" polypeptide or protein is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. In one embodiment, the language "substantially free" means preparation of 57242 protein having less than about 30%, 20%, 10% and more preferably 5% (by dry weight), of non-57242 protein (also referred to herein as a "contaminating protein"), or of chemical precursors or non-57242 chemicals. When the 57242 protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, i.e., culture medium represents less than about 20%,

more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The invention includes isolated or purified preparations of at least 0.01, 0.1, 1.0, and 10 milligrams in dry weight.

[0077] A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of 57242 (e.g., the sequence of SEQ ID NO:1 or SEQ ID NO:3, without abolishing or more preferably, without substantially altering a biological activity, whereas an "essential" amino acid residue results in such a change. For example, amino acid residues that are conserved among the polypeptides of the present invention, e.g., those present in the G protein-coupled receptor domain, are predicted to be particularly unamenable to alteration.

[0078] A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (e.g., lysine, arginine, histidine), acidic side chains (e.g., aspartic acid, glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (e.g., threonine, valine, isoleucine) and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in a 57242 protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a 57242 coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for 57242 biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:1 or SEQ ID NO:3, the encoded protein can be expressed recombinantly and the activity of the protein can be determined.

[0079] As used herein, a "biologically active portion" of a 57242 protein includes a fragment of a 57242 protein which participates in an interaction between a 57242 molecule and a non-57242 molecule. Biologically active portions of a 57242 protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the 57242 protein, e.g., the amino acid sequence shown in SEQ ID NO:2, which include less amino acids than the full length 57242 proteins, and exhibit at least one activity of a 57242 protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the 57242 protein, e.g., G protein-coupled receptor activity. A

biologically active portion of a 57242 protein can be a polypeptide which is, for example, 10, 25, 50, 100, 200 or more amino acids in length. Biologically active portions of a 57242 protein can be used as targets for developing agents which modulate a 57242 mediated activity, e.g., G protein-coupled receptor activity.

**[0080]** Calculations of homology or sequence identity between sequences (the terms are used interchangeably herein) are performed as follows.

**[0081]** To determine the percent identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (e.g., gaps can be introduced in one or both of a first and a second amino acid or nucleic acid sequence for optimal alignment and non-homologous sequences can be disregarded for comparison purposes). In a preferred embodiment, the length of a reference sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 50%, even more preferably at least 60%, and even more preferably at least 70%, 80%, 90%, 100% of the length of the reference sequence (e.g., when aligning a second sequence to the 57242 amino acid sequence of SEQ ID NO:2 having 346 amino acid residues, at least 104, preferably at least 138, more preferably at least 173, even more preferably at least 208, and even more preferably at least 242, 277, 311, or 346 amino acid residues are aligned. The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are identical at that position (as used herein amino acid or nucleic acid "identity" is equivalent to amino acid or nucleic acid "homology"). The percent identity between the two sequences is a function of the number of identical positions shared by the sequences, taking into account the number of gaps, and the length of each gap, which need to be introduced for optimal alignment of the two sequences.

**[0082]** The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (*J. Mol. Biol.* (48):444-453 (1970)) algorithm which has been incorporated into the GAP program in the GCG software package (available at <http://www.gcg.com>), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined

using the GAP program in the GCG software package (available at <http://www.gcg.com>), using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) is using a Blossum 62 scoring matrix with a gap open penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

[0083] The percent identity between two amino acid or nucleotide sequences can be determined using the algorithm of E. Meyers and W. Miller (CABIOS, 4:11-17 (1989)) which has been incorporated into the ALIGN program (version 2.0), using a PAM120 weight residue table, a gap length penalty of 12 and a gap penalty of 4.

[0084] The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, et al., (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 57242 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 57242 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul et al., (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. See <http://www.ncbi.nlm.nih.gov>.

[0085] "Misexpression or aberrant expression", as used herein, refers to a non-wild type pattern of gene expression, at the RNA or protein level. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of decreased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-transitional modification, or biological activity of the expressed polypeptide; a pattern of

expression that differs from wild type in terms of the effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

[0086] "Subject", as used herein, can refer to a mammal, e.g., a human, or to an experimental or animal or disease model. The subject can also be a non-human animal, e.g., a horse, cow, goat, or other domestic animal.

[0087] A "purified preparation of cells", as used herein, refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least 10% and more preferably 50% of the subject cells.

[0088] Various aspects of the invention are described in further detail below.

#### Isolated Nucleic Acid Molecules

[0089] In one aspect, the invention provides, an isolated or purified, nucleic acid molecule that encodes a 57242 polypeptide described herein, e.g., a full length 57242 protein or a fragment thereof, e.g., a biologically active portion of 57242 protein. Also included is a nucleic acid fragment suitable for use as a hybridization probe, which can be used, e.g., to identify nucleic acid molecule encoding a polypeptide of the invention, 57242 mRNA, and fragments suitable for use as primers, e.g., PCR primers for the amplification or mutation of nucleic acid molecules.

[0090] In one embodiment, an isolated nucleic acid molecule of the invention includes the nucleotide sequence shown in SEQ ID NO:1, or a portion of any of these nucleotide sequences. In one embodiment, the nucleic acid molecule includes sequences encoding the human 57242 protein (i.e., "the coding region", from nucleotides 154-1194 of SEQ ID NO:1, not including the terminal codon), as well as 5' untranslated sequences (nucleotides 1-153 of SEQ ID NO:1). Alternatively, the nucleic acid molecule can include only the coding region of SEQ ID NO:1 (e.g., nucleotides 154-1194 of SEQ ID NO:1, corresponding to SEQ ID NO:3) and, e.g., no flanking sequences which normally accompany the subject sequence. In another embodiment, the nucleic acid molecule encodes a sequence corresponding to the mature protein of SEQ ID NO:2.

[0091] In another embodiment, an isolated nucleic acid molecule of the invention includes a nucleic acid molecule which is a complement of the nucleotide sequence shown

in SEQ ID NO:1, SEQ ID NO:3, or a portion of any of these nucleotide sequences. In other embodiments, the nucleic acid molecule of the invention is sufficiently complementary to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3, such that it can hybridize to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3, thereby forming a stable duplex.

**[0092]** In one embodiment, an isolated nucleic acid molecule of the present invention includes a nucleotide sequence which is at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or more homologous to the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. In the case of an isolated nucleic acid molecule which is longer than or equivalent in length to the reference sequence, e.g., SEQ ID NO:1, or SEQ ID NO:3, the comparison is made with the full length of the reference sequence. Where the isolated nucleic acid molecule is shorter than the reference sequence, e.g., shorter than SEQ ID NO:1, or SEQ ID NO:3, the comparison is made to a segment of the reference sequence of the same length (excluding any loop required by the homology calculation).

#### 57242 Nucleic Acid Fragments

**[0093]** A nucleic acid molecule of the invention can include only a portion of the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:3. For example, such a nucleic acid molecule can include a fragment which can be used as a probe or primer or a fragment encoding a portion of a 57242 protein, e.g., an immunogenic or biologically active portion of a 57242 protein. A fragment can comprise: nucleotides 94-834 of SEQ ID NO:1, which encodes an G protein-coupled receptor domain of human 57242. The nucleotide sequence determined from the cloning of the 57242 gene allows for the generation of probes and primers designed for use in identifying and/or cloning other 57242 family members, or fragments thereof, as well as 57242 homologues, or fragments thereof, from other species.

**[0094]** In another embodiment, a nucleic acid includes a nucleotide sequence that includes part, or all, of the coding region and extends into either (or both) the 5' or 3' noncoding region. Other embodiments include a fragment which includes a nucleotide sequence encoding an amino acid fragment described herein. Nucleic acid fragments can encode a specific domain or site described herein or fragments thereof, particularly fragments thereof which are at least 150 amino acids in length. Fragments also include nucleic acid sequences corresponding to specific amino acid sequences described above or fragments thereof. Nucleic acid fragments should not

to be construed as encompassing those fragments that may have been disclosed prior to the invention.

[0095] A nucleic acid fragment can include a sequence corresponding to a domain, region, or functional site described herein. A nucleic acid fragment can also include one or more domain, region, or functional site described herein. Thus, for example, the nucleic acid fragment can include an G protein-coupled receptor domain. In a preferred embodiment the fragment is at least, 50, 100, 200, 300, 400, 500, 600, 700, or 900 base pairs in length.

[0096] 57242 probes and primers are provided. Typically a probe/primer is an isolated or purified oligonucleotide. The oligonucleotide typically includes a region of nucleotide sequence that hybridizes under stringent conditions to at least about 7, 12 or 15, preferably about 20 or 25, more preferably about 30, 35, 40, 45, 50, 55, 60, 65, or 75 consecutive nucleotides of a sense or antisense sequence of SEQ ID NO:1, SEQ ID NO:3, or of a naturally occurring allelic variant or mutant of SEQ ID NO:1 or SEQ ID NO:3.

[0097] In a preferred embodiment the nucleic acid is a probe which is at least 5 or 10, and less than 200, more preferably less than 100, or less than 50, base pairs in length. It should be identical, or differ by 1, or less than in 5 or 10 bases, from a sequence disclosed herein. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[0098] A probe or primer can be derived from the sense or anti-sense strand of a nucleic acid which encodes an G protein-coupled receptor domain (e.g., about amino acid residues 32-278 of SEQ ID NO:2).

[0099] In another embodiment a set of primers is provided, e.g., primers suitable for use in a PCR, which can be used to amplify a selected region of a 57242 sequence, e.g., a region described herein. The primers should be at least 5, 10, or 50 base pairs in length and less than 100, or less than 200, base pairs in length. The primers should be identical, or differs by one base from a sequence disclosed herein or from a naturally occurring variant. E.g., primers suitable for amplifying all or a portion of any of the following regions are provided: an G protein-coupled receptor domain (e.g., about amino acid residues 32-278 of SEQ ID NO:2).

[00100] A nucleic acid fragment can encode an epitope bearing region of a polypeptide described herein.

[00101] A nucleic acid fragment encoding a "biologically active portion of a 57242 polypeptide" can be prepared by isolating a portion of the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3, which encodes a polypeptide having a 57242 biological activity (e.g., the biological activities of the 57242 proteins as described herein), expressing the encoded portion of the 57242 protein (e.g., by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the 57242 protein. For example, a nucleic acid fragment encoding a biologically active portion of 57242 includes an G protein-coupled receptor domain (e.g., about amino acid residues 32-278 of SEQ ID NO:2). A nucleic acid fragment encoding a biologically active portion of a 57242 polypeptide, may comprise a nucleotide sequence which is greater than 300-1200 or more nucleotides in length.

[00102] In preferred embodiments, nucleic acids include a nucleotide sequence which is about 300, 400, 500, 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400 nucleotides in length and hybridizes under stringent hybridization conditions to a nucleic acid molecule of SEQ ID NO:1, or SEQ ID NO:3.

#### 57242 Nucleic Acid Variants

[00103] The invention further encompasses nucleic acid molecules that differ from the nucleotide sequence shown in SEQ ID NO:1 or SEQ ID NO:3. Such differences can be due to degeneracy of the genetic code (and result in a nucleic acid which encodes the same 57242 proteins as those encoded by the nucleotide sequence disclosed herein. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence which differs, by at least 1, but less than 5, 10, 20, 50, or 100 amino acid residues that shown in SEQ ID NO:2. If alignment is needed for this comparison the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[00104] Nucleic acids of the inventor can be chosen for having codons, which are preferred, or non preferred, for a particular expression system. E.g., the nucleic acid can be one in which at least one colon, at preferably at least 10%, or 20% of the codons has been altered such that the sequence is optimized for expression in *E. coli*, yeast, human, insect, or CHO cells.

[00105] Nucleic acid variants can be naturally occurring, such as allelic variants (same locus), homologs (different locus), and orthologs (different organism) or can be non-naturally

occurring. Non-naturally occurring variants can be made by mutagenesis techniques, including those applied to polynucleotides, cells, or organisms. The variants can contain nucleotide substitutions, deletions, inversions and insertions. Variation can occur in either or both the coding and non-coding regions. The variations can produce both conservative and non-conservative amino acid substitutions (as compared in the encoded product).

[00106] In a preferred embodiment, the nucleic acid differs from that of SEQ ID NO:1 or SEQ ID NO:3, e.g., as follows: by at least one but less than 10, 20, 30, or 40 nucleotides; at least one but less than 1%, 5%, 10% or 20% of the in the subject nucleic acid. If necessary for this analysis the sequences should be aligned for maximum homology. "Looped" out sequences from deletions or insertions, or mismatches, are considered differences.

[00107] Orthologs, homologs, and allelic variants can be identified using methods known in the art. These variants comprise a nucleotide sequence encoding a polypeptide that is 50%, at least about 55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically at least about 90-95% or more identical to the amino acid sequence shown in SEQ ID NO:2 or a fragment of this sequence. Such nucleic acid molecules can readily be obtained as being able to hybridize under stringent conditions, to the nucleotide sequence shown in SEQ ID NO:3 or a fragment of this sequence. Nucleic acid molecules corresponding to orthologs, homologs, and allelic variants of the 57242 cDNAs of the invention can further be isolated by mapping to the same chromosome or locus as the 57242 gene. Preferred variants include those that are correlated with G protein-coupled receptor activity.

[00108] Allelic variants of 57242, e.g., human 57242, include both functional and non-functional proteins. Functional allelic variants are naturally occurring amino acid sequence variants of the 57242 protein within a population that maintain the ability to modulate the phosphorylation state of itself or another protein or polypeptide. Functional allelic variants will typically contain only conservative substitution of one or more amino acids of SEQ ID NO:2, or substitution, deletion or insertion of non-critical residues in non-critical regions of the protein. Non-functional allelic variants are naturally-occurring amino acid sequence variants of the 57242, e.g., human 57242, protein within a population that do not have the ability to attach an acyl chain to a lipid precursor. Non-functional allelic variants will typically contain a non-conservative substitution, a deletion, or insertion, or premature truncation of the amino acid sequence of SEQ ID NO:2, or a substitution, insertion, or deletion in critical residues or critical regions of the protein.

[00109] Moreover, nucleic acid molecules encoding other 57242 family members and, thus, which have a nucleotide sequence which differs from the 57242 sequences of SEQ ID NO:1 or SEQ ID NO:3 are intended to be within the scope of the invention.

[00110] Antisense Nucleic Acid Molecules, Ribozymes and Modified 57242 Nucleic Acid Molecules

[00111] In another aspect, the invention features, an isolated nucleic acid molecule which is antisense to 57242. An "antisense" nucleic acid can include a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, e.g., complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. The antisense nucleic acid can be complementary to an entire 57242 coding strand, or to only a portion thereof (e.g., the coding region of human 57242 corresponding to SEQ ID NO:3). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding 57242 (e.g., the 5' and 3' untranslated regions).

[00112] An antisense nucleic acid can be designed such that it is complementary to the entire coding region of 57242 mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of 57242 mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of 57242 mRNA, e.g., between the -10 and +10 regions of the target gene nucleotide sequence of interest. An antisense oligonucleotide can be, for example, about 7, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, or more nucleotides in length.

[00113] An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (e.g., an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, e.g., phosphorothioate derivatives and acridine substituted nucleotides can be used. The antisense nucleic acid also can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (i.e., RNA transcribed from the inserted nucleic acid

will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

[00114] The antisense nucleic acid molecules of the invention are typically administered to a subject (e.g., by direct injection at a tissue site), or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a 57242 protein to thereby inhibit expression of the protein, e.g., by inhibiting transcription and/or translation. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, e.g., by linking the antisense nucleic acid molecules to peptides or antibodies which bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

[00115] In yet another embodiment, the antisense nucleic acid molecule of the invention is an  $\alpha$ -anomeric nucleic acid molecule. An  $\alpha$ -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual  $\beta$ -units, the strands run parallel to each other (Gaultier et al., (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue et al., (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue et al., (1987) *FEBS Lett.* 215:327-330).

[00116] In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. A ribozyme having specificity for a 57242-encoding nucleic acid can include one or more sequences complementary to the nucleotide sequence of a 57242 cDNA disclosed herein (i.e., SEQ ID NO:1, or SEQ ID NO:3), and a sequence having known catalytic sequence responsible for mRNA cleavage (see U.S. Pat. No. 5,093,246 or Haselhoff and Gerlach, (1988) *Nature* 334:585-591). For example, a derivative of a *Tetrahymena* L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a 57242-encoding mRNA. See, e.g., Cech et al. U.S. Patent No. 4,987,071; and Cech et al. U.S. Patent No. 5,116,742. Alternatively, 57242 mRNA can be used to select a catalytic RNA having a specific

ribonuclease activity from a pool of RNA molecules. See, e.g., Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

[00117] 57242 gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the 57242 (e.g., the 57242 promoter and/or enhancers) to form triple helical structures that prevent transcription of the 57242 gene in target cells. See generally, Helene, C., (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. et al., (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J., (1992) *Bioassays* 14(12):807-15. The potential sequences that can be targeted for triple helix formation can be increased by creating a so-called "switchback" nucleic acid molecule. Switchback molecules are synthesized in an alternating 5'-3', 3'-5' manner, such that they base pair with first one strand of a duplex and then the other, eliminating the necessity for a sizeable stretch of either purines or pyrimidines to be present on one strand of a duplex.

[00118] The invention also provides detectably labeled oligonucleotide primer and probe molecules. Typically, such labels are chemiluminescent, fluorescent, radioactive, or colorimetric.

[00119] A 57242 nucleic acid molecule can be modified at the base moiety, sugar moiety or phosphate backbone to improve, e.g., the stability, hybridization, or solubility of the molecule. For example, the deoxyribose phosphate backbone of the nucleic acid molecules can be modified to generate peptide nucleic acids (see Hyrup B. et al., (1996) *Bioorganic & Medicinal Chemistry* 4 (1): 5-23). As used herein, the terms "peptide nucleic acid" or "PNA" refers to a nucleic acid mimic, e.g., a DNA mimic, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of a PNA can allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide synthesis protocols as described in Hyrup B. et al., (1996) *supra*; Perry-O'Keefe et al., *Proc. Natl. Acad. Sci.* 93: 14670-675.

[00120] PNAs of 57242 nucleic acid molecules can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, for example, inducing transcription or translation arrest or inhibiting replication. PNAs of 57242 nucleic acid molecules can also be used in the analysis of single base pair mutations in a gene, (e.g., by PNA-directed PCR clamping); as 'artificial restriction enzymes' when used in combination with other enzymes, (e.g., S1

nucleases (Hyrup B., (1996) *supra*); or as probes or primers for DNA sequencing or hybridization (Hyrup B. et al., (1996) *supra*; Perry-O'Keefe *supra*).

[00121] In other embodiments, the oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:6553-6556; Lemaitre et al., (1987) *Proc. Natl. Acad. Sci. USA* 84:648-652; PCT Publication No. W088/09810) or the blood-brain barrier (see, e.g., PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization-triggered cleavage agents (See, e.g., Krol et al., (1988) *Bio-Techniques* 6:958-976) or intercalating agents. (See, e.g., Zon, (1988) *Pharm. Res.* 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, (e.g., a peptide, hybridization triggered cross-linking agent, transport agent, or hybridization-triggered cleavage agent).

[00122] The invention also includes molecular beacon oligonucleotide primer and probe molecules having at least one region which is complementary to a 57242 nucleic acid of the invention, two complementary regions one having a fluorophore and one a quencher such that the molecular beacon is useful for quantitating the presence of the 57242 nucleic acid of the invention in a sample. Molecular beacon nucleic acids are described, for example, in Lizardi et al., U.S. Patent No. 5,854,033; Nazarenko et al., U.S. Patent No. 5,866,336, and Livak et al., U.S. Patent 5,876,930.

#### Isolated 57242 Polypeptides

[00123] In another aspect, the invention features, an isolated 57242 protein, or fragment, e.g., a biologically active portion, for use as immunogens or antigens to raise or test (or more generally to bind) anti-57242 antibodies. 57242 protein can be isolated from cells or tissue sources using standard protein purification techniques. 57242 protein or fragments thereof can be produced by recombinant DNA techniques or synthesized chemically.

[00124] Polypeptides of the invention include those which arise as a result of the existence of multiple genes, alternative transcription events, alternative RNA splicing events, and alternative translational and posttranslational events. The polypeptide can be expressed in systems, e.g., cultured cells, which result in substantially the same posttranslational modifications present when expressed the polypeptide is expressed in a native cell, or in systems which result in the alteration or omission of posttranslational modifications, e.g., glycosylation or cleavage, present when expressed in a native cell.

**[00125]** In a preferred embodiment, a 57242 polypeptide has one or more of the following characteristics:

it has the ability to regulate, sense and/or transmit an extracellular signal into a cell;

it has the ability to interact with (*e.g.*, bind to) an extracellular signal or a cell surface receptor;

it has the ability to mobilize an intracellular molecule that participates in a signal transduction pathway (*e.g.*, adenylate cyclase or phosphatidylinositol 4,5-bisphosphate (PIP<sub>2</sub>), inositol 1,4,5-triphosphate (IP<sub>3</sub>));

it has the ability to regulate polarization of the plasma membrane;

it has the ability to modulate cell proliferation, cell migration, differentiation and/or cell survival;

it has the ability to modulate function, survival, morphology, proliferation and/or differentiation of cells of tissues in which 57242 molecules are expressed;

it has a molecular weight (*e.g.*, deduced molecular weight), amino acid composition or other physical characteristic of a 57242 protein of SEQ ID NO:2;

it has an overall sequence similarity (identity) of at least 60%, preferably at least 70%, more preferably at least 75, 80, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99% or more, with a polypeptide of SEQ ID NO:2;

it has an N-terminal domain which is preferably about 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher, identical to a polypeptide of SEQ ID NO:2;

it has at least one transmembrane domains which is preferably about 70%, 80%, 90%, 95% or higher, identical to a polypeptide of SEQ ID NO:2;

it has a C-terminal domain which is preferably about 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99% or higher, identical to a polypeptide of SEQ ID NO:2; or

it has an G protein-coupled receptor domain which preferably has an overall sequence similarity of about 70%, 80%, 90% or 95% with amino acid residues 32-278 of SEQ ID NO:2.

**[00126]** In a preferred embodiment the 57242 protein, or fragment thereof, differs from the corresponding sequence in SEQ ID NO:2. In one embodiment it differs by at least one but by less than 15, 10 or 5 amino acid residues. In another it differs from the corresponding sequence in SEQ ID NO:2 by at least one residue but less than 20%, 15%, 10% or 5% of the residues in it differ from the corresponding sequence in SEQ ID NO:2. (If this comparison requires alignment the sequences should be aligned for maximum homology. "Looped" out

sequences from deletions or insertions, or mismatches, are considered differences.) The differences are, preferably, differences or changes at a non-essential residue or a conservative substitution. In a preferred embodiment the differences are not in the G protein-coupled receptor domain. In another preferred embodiment one or more differences are in non-active site residues, e.g. outside of the G protein-coupled receptor domain.

[00127] Other embodiments include a protein that contain one or more changes in amino acid sequence, e.g., a change in an amino acid residue which is not essential for activity. Such 57242 proteins differ in amino acid sequence from SEQ ID NO:2, yet retain biological activity.

[00128] In one embodiment, a biologically active portion of a 57242 protein includes an G protein-coupled receptor domain. In another embodiment, a biologically active portion of a 57242 protein includes a MttB family UPF0032 domain. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native 57242 protein.

[00129] In a preferred embodiment, the 57242 protein has an amino acid sequence shown in SEQ ID NO:2. In other embodiments, the 57242 protein is substantially identical to SEQ ID NO:2. In yet another embodiment, the 57242 protein is substantially identical to SEQ ID NO:2 and retains the functional activity of the protein of SEQ ID NO:2, as described in detail above. Accordingly, in another embodiment, the 57242 protein is a protein which includes an amino acid sequence at least about 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 98% or more identical to SEQ ID NO:2.

#### 57242 Chimeric or Fusion Proteins

[00130] In another aspect, the invention provides 57242 chimeric or fusion proteins. As used herein, a 57242 "chimeric protein" or "fusion protein" includes a 57242 polypeptide linked to a non-57242 polypeptide. A "non-57242 polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the 57242 protein, e.g., a protein which is different from the 57242 protein and which is derived from the same or a different organism. The 57242 polypeptide of the fusion protein can correspond to all or a portion e.g., a fragment described herein of a 57242 amino acid sequence. In a preferred embodiment, a 57242 fusion protein includes at least

one (or two) biologically active portion of a 57242 protein. The non-57242 polypeptide can be fused to the N-terminus or C-terminus of the 57242 polypeptide.

[00131] The fusion protein can include a moiety which has a high affinity for a ligand. For example, the fusion protein can be a GST-57242 fusion protein in which the 57242 sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant 57242. Alternatively, the fusion protein can be a 57242 protein containing a heterologous signal sequence at its N-terminus. In certain host cells (e.g., mammalian host cells), expression and/or secretion of 57242 can be increased through use of a heterologous signal sequence.

[00132] Fusion proteins can include all or a part of a serum protein, e.g., an IgG constant region, or human serum albumin.

[00133] The 57242 fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject *in vivo*. The 57242 fusion proteins can be used to affect the bioavailability of a 57242 substrate. 57242 fusion proteins may be useful therapeutically for the treatment of disorders caused by, for example, (i) aberrant modification or mutation of a gene encoding a 57242 protein; (ii) mis-regulation of the 57242 gene; and (iii) aberrant post-translational modification of a 57242 protein.

[00134] Moreover, the 57242-fusion proteins of the invention can be used as immunogens to produce anti-57242 antibodies in a subject, to purify 57242 ligands and in screening assays to identify molecules which inhibit the interaction of 57242 with a 57242 substrate.

[00135] Expression vectors are commercially available that already encode a fusion moiety (e.g., a GST polypeptide). A 57242-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the 57242 protein.

#### Variants of 57242 Proteins

[00136] In another aspect, the invention also features a variant of a 57242 polypeptide, e.g., which functions as an agonist (mimetics) or as an antagonist. Variants of the 57242 proteins can be generated by mutagenesis, e.g., discrete point mutation, the insertion or deletion of sequences or the truncation of a 57242 protein. An agonist of the 57242 proteins can retain substantially the same, or a subset, of the biological activities of the naturally occurring form of a 57242 protein. An antagonist of a 57242 protein can inhibit one or more of the activities of the naturally occurring form of the 57242 protein by, for example,

competitively modulating a 57242-mediated activity of a 57242 protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. Preferably, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the 57242 protein.

[00137] Variants of a 57242 protein can be identified by screening combinatorial libraries of mutants, e.g., truncation mutants, of a 57242 protein for agonist or antagonist activity.

[00138] Libraries of fragments e.g., N terminal, C terminal, or internal fragments, of a 57242 protein coding sequence can be used to generate a variegated population of fragments for screening and subsequent selection of variants of a 57242 protein.

[00139] Variants in which a cysteine residues is added or deleted or in which a residue which is glycosylated is added or deleted are particularly preferred.

[00140] Methods for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify 57242 variants (Arkin and Yourvan, (1992) *Proc. Natl. Acad. Sci. USA* 89:7811-7815; Delgrave et al., (1993) *Protein Engineering* 6(3):327-331).

[00141] Cell based assays can be exploited to analyze a variegated 57242 library. For example, a library of expression vectors can be transfected into a cell line, e.g., a cell line, which ordinarily responds to 57242 in a substrate-dependent manner. The transfected cells are then contacted with 57242 and the effect of the expression of the mutant on signaling by the 57242 substrate can be detected, e.g., by measuring G protein-coupled receptor activity. Plasmid DNA can then be recovered from the cells which score for inhibition, or alternatively, potentiation of signaling by the 57242 substrate, and the individual clones further characterized.

[00142] In another aspect, the invention features a method of making a 57242 polypeptide, e.g., a peptide having a non-wild type activity, e.g., an antagonist, agonist, or super agonist of a naturally occurring 57242 polypeptide, e.g., a naturally occurring 57242 polypeptide. The method includes: altering the sequence of a 57242 polypeptide, e.g., altering the sequence, e.g., by substitution or deletion of one or more residues of a non-conserved region, a domain or residue disclosed herein, and testing the altered polypeptide for the desired activity.

[00143] In another aspect, the invention features a method of making a fragment or analog of a 57242 polypeptide a biological activity of a naturally occurring 57242 polypeptide. The method includes: altering the sequence, e.g., by substitution or deletion of one or more residues, of a 57242 polypeptide, e.g., altering the sequence of a non-conserved region, or a domain or residue described herein, and testing the altered polypeptide for the desired activity.

#### Anti-57242 Antibodies

[00144] In another aspect, the invention provides an anti-57242 antibody. The term "antibody" as used herein refers to an immunoglobulin molecule or immunologically active portion thereof, i.e., an antigen-binding portion. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')<sub>2</sub> fragments which can be generated by treating the antibody with an enzyme such as pepsin.

[00145] The antibody can be a polyclonal, monoclonal, recombinant, e.g., a chimeric or humanized, fully human, non-human, e.g., murine, or single chain antibody. In a preferred embodiment it has effector function and can fix complement. The antibody can be coupled to a toxin or imaging agent.

[00146] A full-length 57242 protein or, antigenic peptide fragment of 57242 can be used as an immunogen or can be used to identify anti-57242 antibodies made with other immunogens, e.g., cells, membrane preparations, and the like. The antigenic peptide of 57242 should include at least 8 amino acid residues of the amino acid sequence shown in SEQ ID NO:2 and encompasses an epitope of 57242. Preferably, the antigenic peptide includes at least 10 amino acid residues, more preferably at least 15 amino acid residues, even more preferably at least 20 amino acid residues, and most preferably at least 30 amino acid residues.

[00147] Fragments of 57242 which include, e.g., residues 296-316 of SEQ ID NO:2 can be, e.g., used as immunogens, or used to characterize the specificity of an antibody or antibodies against what are believed to be hydrophilic regions of the 57242 protein. Similarly, a fragment of 57242 which includes, e.g., residues 221-251 of SEQ ID NO:2 can be used to make an antibody against what is believed to be a hydrophobic region of the 57242 protein; a fragment of 57242 which includes residues 32-278 of SEQ ID NO:2 can be used to make an antibody against the G protein-coupled receptor region of the 57242 protein.

[00148] Antibodies reactive with, or specific for, any of these regions, or other regions or domains described herein are provided.

[00149] In a preferred embodiment the antibody fails to bind an Fc receptor, e.g. it is a type which does not support Fc receptor binding or has been modified, e.g., by deletion or other mutation, such that it does not have a functional Fc receptor binding region.

[00150] Preferred epitopes encompassed by the antigenic peptide are regions of 57242 are located on the surface of the protein, e.g., hydrophilic regions, as well as regions with high antigenicity. For example, an Emini surface probability analysis of the human 57242 protein sequence can be used to indicate the regions that have a particularly high probability of being localized to the surface of the 57242 protein and are thus likely to constitute surface residues useful for targeting antibody production.

[00151] In a preferred embodiment the antibody binds an epitope on any domain or region on 57242 proteins described herein.

[00152] Chimeric, humanized, but most preferably, completely human antibodies are desirable for applications which include repeated administration, e.g., therapeutic treatment (and some diagnostic applications) of human patients.

[00153] The anti-57242 antibody can be a single chain antibody. A single-chain antibody (scFV) may be engineered (see, for example, Colcher, D. et al., *Ann. NY Acad. Sci.* 1999 Jun 30;880:263-80; and Reiter, Y., *Clin. Cancer Res.* 1996 Feb;2(2):245-52). The single chain antibody can be dimerized or multimerized to generate multivalent antibodies having specificities for different epitopes of the same target 57242 protein.

[00154] An anti-57242 antibody (e.g., monoclonal antibody) can be used to isolate 57242 by standard techniques, such as affinity chromatography or immunoprecipitation.

Moreover, an anti-57242 antibody can be used to detect 57242 protein (e.g., in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the protein. Anti-57242 antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, e.g., to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (i.e., physically linking) the antibody to a detectable substance (i.e., antibody labeling). Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase,  $\alpha$ -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include

streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{35}\text{S}$  or  $^{3}\text{H}$ .

Recombinant Expression Vectors, Host Cells and Genetically Engineered Cells

[00155] In another aspect, the invention includes, vectors, preferably expression vectors, containing a nucleic acid encoding a polypeptide described herein. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked and can include a plasmid, cosmid or viral vector. The vector can be capable of autonomous replication or it can integrate into a host DNA. Viral vectors include, e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses.

[00156] A vector can include a 57242 nucleic acid in a form suitable for expression of the nucleic acid in a host cell. Preferably the recombinant expression vector includes one or more regulatory sequences operatively linked to the nucleic acid sequence to be expressed. The term "regulatory sequence" includes promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence, as well as tissue-specific regulatory and/or inducible sequences. The design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, and the like. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or polypeptides, including fusion proteins or polypeptides, encoded by nucleic acids as described herein (e.g., 57242 proteins, mutant forms of 57242 proteins, fusion proteins, and the like).

[00157] The recombinant expression vectors of the invention can be designed for expression of 57242 proteins in prokaryotic or eukaryotic cells. For example, polypeptides of the invention can be expressed in *E. coli*, insect cells (e.g., using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

[00158] Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S., (1988) *Gene* **67**:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

[00159] Purified fusion proteins can be used in 57242 activity assays, (e.g., direct assays or competitive assays described in detail below), or to generate antibodies specific for 57242 proteins. In a preferred embodiment, a fusion protein expressed in a retroviral expression vector of the present invention can be used to infect bone marrow cells which are subsequently transplanted into irradiated recipients. The pathology of the subject recipient is then examined after sufficient time has passed (e.g., six (6) weeks).

[00160] To maximize recombinant protein expression in *E. coli* is to express the protein in host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* **185**, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in *E. coli* (Wada et al., (1992) *Nucleic Acids Res.* **20**:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

[00161] The 57242 expression vector can be a yeast expression vector, a vector for expression in insect cells, e.g., a baculovirus expression vector or a vector suitable for expression in mammalian cells.

[00162] When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40.

[00163] In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (e.g., tissue-specific regulatory elements are used to express the nucleic acid). Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert et al., (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton, (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore, (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji et al., (1983) *Cell* 33:729-740; Queen and Baltimore, (1983) *Cell* 33:741-748), neuron-specific promoters (e.g., the neurofilament promoter; Byrne and Ruddle, (1989) *Proc. Natl. Acad. Sci. USA* 86:5473-5477), pancreas-specific promoters (Edlund et al., (1985) *Science* 230:912-916), and mammary gland-specific promoters (e.g., milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166).

Developmentally-regulated promoters are also encompassed, for example, the murine hox promoters (Kessel and Gruss, (1990) *Science* 249:374-379) and the  $\alpha$ -fetoprotein promoter (Campes and Tilghman, (1989) *Genes Dev.* 3:537-546).

[00164] The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. Regulatory sequences (e.g., viral promoters and/or enhancers) operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the constitutive, tissue specific or cell type specific expression of antisense RNA in a variety of cell types. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. et al., Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) 1986.

[00165] Another aspect the invention provides a host cell which includes a nucleic acid molecule described herein, e.g., a 57242 nucleic acid molecule within a recombinant expression vector or a 57242 nucleic acid molecule containing sequences which allow it to homologously recombine into a specific site of the host cell's genome. The terms "host cell" and "recombinant host cell" are used interchangeably herein. Such terms refer not only to the particular subject cell but rather also to the progeny or potential progeny of such a cell.

Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[00166] A host cell can be any prokaryotic or eukaryotic cell. For example, a 57242 protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

[00167] Vector DNA can be introduced into host cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (e.g., DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation.

[00168] A host cell of the invention can be used to produce (i.e., express) a 57242 protein. Accordingly, the invention further provides methods for producing a 57242 protein using the host cells of the invention. In one embodiment, the method includes culturing the host cell of the invention (into which a recombinant expression vector encoding a 57242 protein has been introduced) in a suitable medium such that a 57242 protein is produced. In another embodiment, the method further includes isolating a 57242 protein from the medium or the host cell.

[00169] In another aspect, the invention features, a cell or purified preparation of cells which include a 57242 transgene, or which otherwise misexpress 57242. The cell preparation can consist of human or non-human cells, e.g., rodent cells, e.g., mouse or rat cells, rabbit cells, or pig cells. In preferred embodiments, the cell or cells include a 57242 transgene, e.g., a heterologous form of a 57242, e.g., a gene derived from humans (in the case of a non-human cell). The 57242 transgene can be misexpressed, e.g., overexpressed or underexpressed. In other preferred embodiments, the cell or cells include a gene which misexpress an endogenous 57242, e.g., a gene the expression of which is disrupted, e.g., a knockout. Such cells can serve as a model for studying disorders which are related to mutated or mis-expressed 57242 alleles or for use in drug screening.

[00170] In another aspect, the invention features, a human cell, e.g., a hematopoietic stem cell, transformed with nucleic acid which encodes a subject 57242 polypeptide.

[00171] Also provided are cells or a purified preparation thereof, e.g., human cells, in which an endogenous 57242 is under the control of a regulatory sequence that does not

normally control the expression of the endogenous 57242 gene. The expression characteristics of an endogenous gene within a cell, e.g., a cell line or microorganism, can be modified by inserting a heterologous DNA regulatory element into the genome of the cell such that the inserted regulatory element is operably linked to the endogenous 57242 gene. For example, an endogenous 57242 gene, e.g., a gene which is "transcriptionally silent," e.g., not normally expressed, or expressed only at very low levels, may be activated by inserting a regulatory element which is capable of promoting the expression of a normally expressed gene product in that cell. Techniques such as targeted homologous recombinations, can be used to insert the heterologous DNA as described in, e.g., Chappel, US 5,272,071; WO 91/06667, published on May 16, 1991.

#### Transgenic Animals

[00172] The invention provides non-human transgenic animals. Such animals are useful for studying the function and/or activity of a 57242 protein and for identifying and/or evaluating modulators of 57242 activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, and the like. A transgene is exogenous DNA or a rearrangement, e.g., a deletion of endogenous chromosomal DNA, which preferably is integrated into or occurs in the genome of the cells of a transgenic animal. A transgene can direct the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal, other transgenes, e.g., a knockout, reduce expression. Thus, a transgenic animal can be one in which an endogenous 57242 gene has been altered by, e.g., by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

[00173] Intrinsic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to a transgene of the invention to direct expression of a 57242 protein to particular cells. A transgenic founder animal can be identified based upon the presence of a 57242 transgene in its genome and/or expression of 57242 mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals

carrying a transgene encoding a 57242 protein can further be bred to other transgenic animals carrying other transgenes.

[00174] 57242 proteins or polypeptides can be expressed in transgenic animals or plants, e.g., a nucleic acid encoding the protein or polypeptide can be introduced into the genome of an animal. In preferred embodiments the nucleic acid is placed under the control of a tissue specific promoter, e.g., a milk or egg specific promoter, and recovered from the milk or eggs produced by the animal. Suitable animals are mice, pigs, cows, goats, and sheep.

[00175] The invention also includes a population of cells from a transgenic animal, as discussed herein.

#### Uses

[00176] The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: a) screening assays; b) predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenetics); and c) methods of treatment (e.g., therapeutic and prophylactic). In particularly preferred embodiments, the compositions provided herein are used in conjunction with methods of diagnosis and treatment of metabolic disorders (e.g., obesity, hyperlipidemia, diabetes, anorexia, and cachexia).

[00177] The isolated nucleic acid molecules of the invention can be used, for example, to express a 57242 protein (e.g., via a recombinant expression vector in a host cell in gene therapy applications), to detect a 57242 mRNA (e.g., in a biological sample such as adipose tissue) or a genetic alteration in a 57242 gene, and to modulate 57242 activity, as described further below. The 57242 proteins can be used to treat disorders characterized by insufficient or excessive production of a 57242 substrate or production of 57242 inhibitors (e.g., a metabolic disorder). In addition, the 57242 proteins can be used to screen for naturally occurring 57242 substrates, to screen for drugs or compounds which modulate 57242 activity, as well as to treat disorders characterized by insufficient or excessive production of 57242 protein or production of 57242 protein forms which have decreased, aberrant or unwanted activity compared to 57242 wild-type protein. Such disorders include those characterized by aberrant signaling or aberrant, e.g., hyperproliferative, cell growth. Moreover, the anti-57242 antibodies of the invention can be used to detect and isolate 57242 proteins, regulate the bioavailability of 57242 proteins, and modulate 57242 activity.

[00178] A method of evaluating a compound for the ability to interact with, e.g., bind, a subject 57242 polypeptide is provided. The method includes: contacting the compound with the subject 57242 polypeptide; and evaluating ability of the compound to interact with, e.g., to bind or form a complex with the subject 57242 polypeptide. This method can be performed in vitro, e.g., in a cell free system, or *in vivo*, e.g., in a two-hybrid interaction trap assay. This method can be used to identify naturally occurring molecules which interact with subject 57242 polypeptide. It can also be used to find natural or synthetic inhibitors of subject 57242 polypeptide. Screening methods are discussed in more detail below.

**Screening Assays:**

[00179] The invention provides methods (also referred to herein as "screening assays") for identifying modulators, i.e., candidate or test compounds or agents (e.g., proteins, peptides, peptidomimetics, peptoids, small molecules or other drugs) which bind to 57242 proteins, have a stimulatory or inhibitory effect on, for example, 57242 expression or 57242 activity, or have a stimulatory or inhibitory effect on, for example, the expression or activity of a 57242 substrate. Compounds thus identified can be used to modulate the activity of target gene products (e.g., 57242 genes) in a therapeutic protocol, to elaborate the biological function of the target gene product, or to identify compounds that disrupt normal target gene interactions.

[00180] In one embodiment, the invention provides assays for screening candidate or test compounds which are substrates of a 57242 protein or polypeptide or a biologically active portion thereof. In another embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a 57242 protein or polypeptide or a biologically active portion thereof.

[00181] The test compounds of the present invention can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; peptoid libraries [libraries of molecules having the functionalities of peptides, but with a novel, non-peptide backbone which are resistant to enzymatic degradation but which nevertheless remain bioactive] (see, e.g., Zuckermann, R.N. et al., *J. Med. Chem.* 1994, **37**: 2678-85); spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library and peptoid library approaches are limited to peptide libraries, while the

other four approaches are applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S. (1997) *Anticancer Drug Des.* 12:145).

[00182] Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc. Natl. Acad. Sci. U.S.A.* 90:6909; Erb *et al.*, (1994) *Proc. Natl. Acad. Sci. USA* 91:11422; Zuckermann *et al.*, (1994). *J. Med. Chem.* 37:2678; Cho *et al.*, (1993) *Science* 261:1303; Carrell *et al.*, (1994) *Angew. Chem. Int. Ed. Engl.* 33:2059; Carell *et al.*, (1994) *Angew. Chem. Int. Ed. Engl.* 33:2061; and in Gallop *et al.*, (1994) *J. Med. Chem.* 37:1233.

[00183] Libraries of compounds may be presented in solution (e.g., Houghten, (1992) *Biotechniques* 13:412-421), or on beads (Lam, (1991) *Nature* 354:82-84), chips (Fodor, (1993) *Nature* 364:555-556), bacteria or spores (Ladner, United States Patent No. 5,223,409), plasmids (Cull *et al.*, (1992) *Proc. Natl. Acad. Sci. USA* 89:1865-1869) or on phage (Scott and Smith, (1990) *Science* 249:386-390); (Devlin, (1990) *Science* 249:404-406); (Cwirla *et al.*, (1990) *Proc. Natl. Acad. Sci.* 87:6378-6382); (Felici, (1991) *J. Mol. Biol.* 222:301-310); (Ladner *supra*).

[00184] In one embodiment, an assay is a cell-based assay in which a cell which expresses a 57242 protein or biologically active portion thereof is contacted with a test compound, and the ability of the test compound to modulate 57242 activity is determined. Determining the ability of the test compound to modulate 57242 activity can be accomplished by monitoring, for example, G protein-coupled receptor activity. The cell, for example, can be of mammalian origin, e.g., human. Cell homogenates, or fractions, preferably membrane containing fractions, can also be tested.

[00185] The ability of the test compound to modulate 57242 binding to a compound, e.g., a 57242 substrate, or to bind to 57242 can also be evaluated. This can be accomplished, for example, by coupling the compound, e.g., the substrate, with a radioisotope or enzymatic label such that binding of the compound, e.g., the substrate, to 57242 can be determined by detecting the labeled compound, e.g., substrate, in a complex. Alternatively, 57242 could be coupled with a radioisotope or enzymatic label to monitor the ability of a test compound to modulate 57242 binding to a 57242 substrate in a complex. For example, compounds (e.g., 57242 substrates) can be labeled with  $^{125}\text{I}$ ,  $^{35}\text{S}$ ,  $^{14}\text{C}$ , or  $^3\text{H}$ , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, compounds can be enzymatically labeled with, for example,

horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product.

[00186] The ability of a compound (e.g., a 57242 substrate) to interact with 57242 with or without the labeling of any of the interactants can be evaluated. For example, a microphysiometer can be used to detect the interaction of a compound with 57242 without the labeling of either the compound or the 57242. McConnell, H. M. et al., (1992) *Science* 257:1906-1912. As used herein, a "microphysiometer" (e.g., Cytosensor) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between a compound and 57242.

[00187] In yet another embodiment, a cell-free assay is provided in which a 57242 protein or biologically active portion thereof is contacted with a test compound and the ability of the test compound to bind to the 57242 protein or biologically active portion thereof is evaluated. Preferred biologically active portions of the 57242 proteins to be used in assays of the present invention include fragments which participate in interactions with non-57242 molecules, e.g., fragments with high surface probability scores.

[00188] Soluble and/or membrane-bound forms of isolated proteins (e.g., 57242 proteins or biologically active portions thereof) can be used in the cell-free assays of the invention. When membrane-bound forms of the protein are used, it may be desirable to utilize a solubilizing agent. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton® X-100, Triton® X-114, Thesit®, Isotridecypoly(ethylene glycol ether)<sub>n</sub>, 3-[(3-cholamidopropyl)dimethylamminio]-1-propane sulfonate (CHAPS), 3-[(3-cholamidopropyl)dimethylamminio]-2-hydroxy-1-propane sulfonate (CHAPSO), or N-dodecyl-N,N-dimethyl-3-ammonio-1-propane sulfonate.

[00189] Cell-free assays involve preparing a reaction mixture of the target gene protein and the test compound under conditions and for a time sufficient to allow the two components to interact and bind, thus forming a complex that can be removed and/or detected.

[00190] In one embodiment, assays are performed where the ability of an agent to block G protein-coupled receptor activity within a cell is evaluated.

[00191] The interaction between two molecules can also be detected, e.g., using fluorescence energy transfer (FET) (see, for example, Lakowicz *et al.*, U.S. Patent No.

5,631,169; Stavrianopoulos, et al., U.S. Patent No. 4,868,103). A fluorophore label on the first, 'donor' molecule is selected such that its emitted fluorescent energy will be absorbed by a fluorescent label on a second, 'acceptor' molecule, which in turn is able to fluoresce due to the absorbed energy. Alternately, the 'donor' protein molecule may simply utilize the natural fluorescent energy of tryptophan residues. Labels are chosen that emit different wavelengths of light, such that the 'acceptor' molecule label may be differentiated from that of the 'donor'. Since the efficiency of energy transfer between the labels is related to the distance separating the molecules, the spatial relationship between the molecules can be assessed. In a situation in which binding occurs between the molecules, the fluorescent emission of the 'acceptor' molecule label in the assay should be maximal. An FET binding event can be conveniently measured through standard fluorometric detection means well known in the art (e.g., using a fluorimeter).

[00192] In another embodiment, determining the ability of the 57242 protein to bind to a target molecule can be accomplished using real-time Biomolecular Interaction Analysis (BIA) (see, e.g., Sjolander, S. and Urbaniczky, C., (1991) *Anal. Chem.* 63:2338-2345 and Szabo et al., (1995) *Curr. Opin. Struct. Biol.* 5:699-705). "Surface plasmon resonance" or "BIA" detects biospecific interactions in real time, without labeling any of the interactants (e.g., BIACore). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

[00193] In one embodiment, the target gene product or the test substance is anchored onto a solid phase. The target gene product/test compound complexes anchored on the solid phase can be detected at the end of the reaction. Preferably, the target gene product can be anchored onto a solid surface, and the test compound, (which is not anchored), can be labeled, either directly or indirectly, with detectable labels discussed herein.

[00194] It may be desirable to immobilize either 57242, an anti-57242 antibody or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a 57242 protein, or interaction of a 57242 protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which

adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/57242 fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or 57242 protein, and the mixture incubated under conditions conducive to complex formation (e.g., at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of 57242 binding or activity determined using standard techniques.

[00195] Other techniques for immobilizing either a 57242 protein or a target molecule on matrices include using conjugation of biotin and streptavidin. Biotinylated 57242 protein or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques known in the art (e.g., biotinylation kit, Pierce Chemicals, Rockford, IL), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical).

[00196] In order to conduct the assay, the non-immobilized component is added to the coated surface containing the anchored component. After the reaction is complete, unreacted components are removed (e.g., by washing) under conditions such that any complexes formed will remain immobilized on the solid surface. The detection of complexes anchored on the solid surface can be accomplished in a number of ways. Where the previously non-immobilized component is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the previously non-immobilized component is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the immobilized component (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody).

[00197] In one embodiment, this assay is performed utilizing antibodies reactive with 57242 protein or target molecules but which do not interfere with binding of the 57242 protein to its target molecule. Such antibodies can be derivatized to the wells of the plate, and unbound target or 57242 protein trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the 57242

protein or target molecule, as well as enzyme-linked assays which rely on detecting an enzymatic activity associated with the 57242 protein or target molecule.

[00198] Alternatively, cell free assays can be conducted in a liquid phase. In such an assay, the reaction products are separated from unreacted components, by any of a number of standard techniques, including but not limited to: differential centrifugation (see, for example, Rivas, G., and Minton, A.P., *Trends Biochem Sci* 1993 Aug;18(8):284-7); chromatography (gel filtration chromatography, ion-exchange chromatography); electrophoresis (see, e.g., Ausubel, F. et al., eds. *Current Protocols in Molecular Biology* 1999, J. Wiley: New York.); and immunoprecipitation (see, for example, Ausubel, F. et al., eds. *Current Protocols in Molecular Biology* 1999, J. Wiley: New York). Such resins and chromatographic techniques are known to one skilled in the art (see, e.g., Heegaard, N.H., *J Mol. Recognit.* 1998 Winter;11(1-6):141-8; Hage, D.S., and Tweed, S.A., *J. Chromatogr. B Biomed. Sci. Appl.* 1997 Oct 10;699(1-2):499-525). Further, fluorescence energy transfer may also be conveniently utilized, as described herein, to detect binding without further purification of the complex from solution.

[00199] In a preferred embodiment, the assay includes contacting the 57242 protein or biologically active portion thereof with a known compound which binds 57242 to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a 57242 protein, wherein determining the ability of the test compound to interact with a 57242 protein includes determining the ability of the test compound to preferentially bind to 57242 or biologically active portion thereof, or to modulate the activity of a target molecule, as compared to the known compound.

[00200] The target gene products of the invention can, *in vivo*, interact with one or more cellular or extracellular macromolecules, such as proteins. For the purposes of this discussion, such cellular and extracellular macromolecules are referred to herein as "binding partners." Compounds that disrupt such interactions can be useful in regulating the activity of the target gene product. Such compounds can include, but are not limited to molecules such as antibodies, peptides, and small molecules. The preferred target genes/products for use in this embodiment are the 57242 genes herein identified. In an alternative embodiment, the invention provides methods for determining the ability of the test compound to modulate the activity of a 57242 protein through modulation of the activity of a downstream effector of a 57242 target molecule. For example, the activity of the effector molecule on an

appropriate target can be determined, or the binding of the effector to an appropriate target can be determined, as previously described.

[00201] To identify compounds that interfere with the interaction between the target gene product and its cellular or extracellular binding partner(s), e.g., a substrate, a reaction mixture containing the target gene product and the binding partner is prepared, under conditions and for a time sufficient, to allow the two products to form complex. In order to test an inhibitory agent, the reaction mixture is provided in the presence and absence of the test compound. The test compound can be initially included in the reaction mixture, or can be added at a time subsequent to the addition of the target gene and its cellular or extracellular binding partner. Control reaction mixtures are incubated without the test compound or with a placebo. The formation of any complexes between the target gene product and the cellular or extracellular binding partner is then detected. The formation of a complex in the control reaction, but not in the reaction mixture containing the test compound, indicates that the compound interferes with the interaction of the target gene product and the interactive binding partner. Additionally, complex formation within reaction mixtures containing the test compound and normal target gene product can also be compared to complex formation within reaction mixtures containing the test compound and mutant target gene product. This comparison can be important in those cases wherein it is desirable to identify compounds that disrupt interactions of mutant but not normal target gene products.

[00202] These assays can be conducted in a heterogeneous or homogeneous format. Heterogeneous assays involve anchoring either the target gene product or the binding partner onto a solid phase, and detecting complexes anchored on the solid phase at the end of the reaction. In homogeneous assays, the entire reaction is carried out in a liquid phase. In either approach, the order of addition of reactants can be varied to obtain different information about the compounds being tested. For example, test compounds that interfere with the interaction between the target gene products and the binding partners, e.g., by competition, can be identified by conducting the reaction in the presence of the test substance. Alternatively, test compounds that disrupt preformed complexes, e.g., compounds with higher binding constants that displace one of the components from the complex, can be tested by adding the test compound to the reaction mixture after complexes have been formed. The various formats are briefly described below.

[00203] In a heterogeneous assay system, either the target gene product or the interactive cellular or extracellular binding partner, is anchored onto a solid surface (e.g., a microtiter plate), while the non-anchored species is labeled, either directly or indirectly. The anchored species can be immobilized by non-covalent or covalent attachments. Alternatively, an immobilized antibody specific for the species to be anchored can be used to anchor the species to the solid surface.

[00204] In order to conduct the assay, the partner of the immobilized species is exposed to the coated surface with or without the test compound. After the reaction is complete, unreacted components are removed (e.g., by washing) and any complexes formed will remain immobilized on the solid surface. Where the non-immobilized species is pre-labeled, the detection of label immobilized on the surface indicates that complexes were formed. Where the non-immobilized species is not pre-labeled, an indirect label can be used to detect complexes anchored on the surface; e.g., using a labeled antibody specific for the initially non-immobilized species (the antibody, in turn, can be directly labeled or indirectly labeled with, e.g., a labeled anti-Ig antibody). Depending upon the order of addition of reaction components, test compounds that inhibit complex formation or that disrupt preformed complexes can be detected.

[00205] Alternatively, the reaction can be conducted in a liquid phase in the presence or absence of the test compound, the reaction products separated from unreacted components, and complexes detected; e.g., using an immobilized antibody specific for one of the binding components to anchor any complexes formed in solution, and a labeled antibody specific for the other partner to detect anchored complexes. Again, depending upon the order of addition of reactants to the liquid phase, test compounds that inhibit complex or that disrupt preformed complexes can be identified.

[00206] In an alternate embodiment of the invention, a homogeneous assay can be used. For example, a preformed complex of the target gene product and the interactive cellular or extracellular binding partner product is prepared in that either the target gene products or their binding partners are labeled, but the signal generated by the label is quenched due to complex formation (see, e.g., U.S. Patent No. 4,109,496 that utilizes this approach for immunoassays). The addition of a test substance that competes with and displaces one of the species from the preformed complex will result in the generation of a signal above background. In this way, test substances that disrupt target gene product-binding partner interaction can be identified.

[00207] In yet another aspect, the 57242 proteins can be used as "bait proteins" in a two-hybrid assay or three-hybrid assay (see, e.g., U.S. Patent No. 5,283,317; Zervos et al., (1993) *Cell* 72:223-232; Madura et al., (1993) *J. Biol. Chem.* 268:12046-12054; Bartel et al., (1993) *Biotechniques* 14:920-924; Iwabuchi et al., (1993) *Oncogene* 8:1693-1696; and Brent WO94/10300), to identify other proteins, which bind to or interact with 57242 ("57242-binding proteins" or "57242-bp") and are involved in 57242 activity. Such 57242-bps can be activators or inhibitors of signals by the 57242 proteins or 57242 targets as, for example, downstream elements of a 57242-mediated signaling pathway.

[00208] The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for a 57242 protein is fused to a gene encoding the DNA binding domain of a known transcription factor (e.g., GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. (Alternatively the 57242 protein can be fused to the activator domain.) If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a 57242-dependent complex, the DNA-binding and activation domains of the transcription factor are brought into close proximity. This proximity allows transcription of a reporter gene (e.g., LacZ) which is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene which encodes the protein which interacts with the 57242 protein.

[00209] In another embodiment, modulators of 57242 expression are identified. For example, a cell or cell free mixture is contacted with a candidate compound and the expression of 57242 mRNA or protein evaluated relative to the level of expression of 57242 mRNA or protein in the absence of the candidate compound. When expression of 57242 mRNA or protein is greater in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of 57242 mRNA or protein expression. Alternatively, when expression of 57242 mRNA or protein is less (statistically significantly less) in the presence of the candidate compound than in its absence, the candidate compound is identified as an inhibitor of 57242 mRNA or protein expression. The level of 57242

mRNA or protein expression can be determined by methods described herein for detecting 57242 mRNA or protein.

[00210] In another aspect, the invention pertains to a combination of two or more of the assays described herein. For example, a modulating agent can be identified using a cell-based or a cell free assay, and the ability of the agent to modulate the activity of a 57242 protein can be confirmed *in vivo*, e.g., in an animal.

[00211] This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein (e.g., a 57242 modulating agent, an antisense 57242 nucleic acid molecule, a 57242-specific antibody, or a 57242-binding partner) in an appropriate animal model to determine the efficacy, toxicity, side effects, or mechanism of action, of treatment with such an agent. Furthermore, novel agents identified by the above-described screening assays can be used for treatments as described herein.

#### Detection Assays

[00212] Portions or fragments of the nucleic acid sequences identified herein can be used as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome e.g., to locate gene regions associated with genetic disease or to associate 57242 with a disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. These applications are described in the subsections below.

#### Chromosome Mapping

[00213] The 57242 nucleotide sequences or portions thereof can be used to map the location of the 57242 genes on a chromosome. This process is called chromosome mapping. Chromosome mapping is useful in correlating the 57242 sequences with genes associated with disease.

[00214] Briefly, 57242 genes can be mapped to chromosomes by preparing PCR primers (preferably 15-25 bp in length) from the 57242 nucleotide sequences. These primers can then be used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to the 57242 sequences will yield an amplified fragment.

[00215] A panel of somatic cell hybrids in which each cell line contains either a single human chromosome or a small number of human chromosomes, and a full set of mouse chromosomes, can allow easy mapping of individual genes to specific human chromosomes.

(D'Eustachio P. et al., (1983) *Science* 220:919-924).

[00216] Other mapping strategies e.g., *in situ* hybridization (described in Fan, Y. et al., (1990) *Proc. Natl. Acad. Sci. USA*, 87:6223-27), pre-screening with labeled flow-sorted chromosomes, and pre-selection by hybridization to chromosome specific cDNA libraries can be used to map 57242 to a chromosomal location.

[00217] Fluorescence *in situ* hybridization (FISH) of a DNA sequence to a metaphase chromosomal spread can further be used to provide a precise chromosomal location in one step. The FISH technique can be used with a DNA sequence as short as 500 or 600 bases. However, clones larger than 1,000 bases have a higher likelihood of binding to a unique chromosomal location with sufficient signal intensity for simple detection. Preferably 1,000 bases, and more preferably 2,000 bases will suffice to get good results at a reasonable amount of time. For a review of this technique, see Verma et al., *Human Chromosomes: A Manual of Basic Techniques* (Pergamon Press, New York 1988).

[00218] Reagents for chromosome mapping can be used individually to mark a single chromosome or a single site on that chromosome, or panels of reagents can be used for marking multiple sites and/or multiple chromosomes. Reagents corresponding to noncoding regions of the genes actually are preferred for mapping purposes. Coding sequences are more likely to be conserved within gene families, thus increasing the chance of cross hybridizations during chromosomal mapping.

[00219] Once a sequence has been mapped to a precise chromosomal location, the physical position of the sequence on the chromosome can be correlated with genetic map data. (Such data are found, for example, in V. McKusick, *Mendelian Inheritance in Man*, available on-line through Johns Hopkins University Welch Medical Library). The relationship between a gene and a disease, mapped to the same chromosomal region, can then be identified through linkage analysis (co-inheritance of physically adjacent genes), described in, for example, Egeland, J. et al., (1987) *Nature*, 325:783-787.

[00220] Moreover, differences in the DNA sequences between individuals affected and unaffected with a disease associated with the 57242 gene, can be determined. If a mutation is observed in some or all of the affected individuals but not in any unaffected individuals, then the mutation is likely to be the causative agent of the particular disease. Comparison of

affected and unaffected individuals generally involves first looking for structural alterations in the chromosomes, such as deletions or translocations that are visible from chromosome spreads or detectable using PCR based on that DNA sequence. Ultimately, complete sequencing of genes from several individuals can be performed to confirm the presence of a mutation and to distinguish mutations from polymorphisms.

Tissue Typing

**[00221]** 57242 sequences can be used to identify individuals from biological samples using, e.g., restriction fragment length polymorphism (RFLP). In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, the fragments separated, e.g., in a Southern blot, and probed to yield bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP (described in U.S. Patent 5,272,057).

**[00222]** Furthermore, the sequences of the present invention can also be used to determine the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the 57242 nucleotide sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it. Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences.

**[00223]** Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:1 can provide positive individual identification with a panel of perhaps 10 to 1,000 primers which each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences, such as those in SEQ ID NO:3 are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

**[00224]** If a panel of reagents from 57242 nucleotide sequences described herein is used to generate a unique identification database for an individual, those same reagents can later be used to identify tissue from that individual. Using the unique identification database,

positive identification of the individual, living or dead, can be made from extremely small tissue samples.

#### Use of Partial 57242 Sequences in Forensic Biology

[00225] DNA-based identification techniques can also be used in forensic biology. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, or semen found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

[00226] The sequences of the present invention can be used to provide polynucleotide reagents, e.g., PCR primers, targeted to specific loci in the human genome, which can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (i.e. another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NO:1 (e.g., fragments derived from the noncoding regions of SEQ ID NO:1 having a length of at least 20 bases, preferably at least 30 bases) are particularly appropriate for this use.

[00227] The 57242 nucleotide sequences described herein can further be used to provide polynucleotide reagents, e.g., labeled or labelable probes which can be used in, for example, an *in situ* hybridization technique, to identify a specific tissue, e.g., a tissue containing G protein-coupled receptor activity. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such 57242 probes can be used to identify tissue by species and/or by organ type.

[00228] In a similar fashion, these reagents, e.g., 57242 primers or probes can be used to screen tissue culture for contamination (i.e. screen for the presence of a mixture of different types of cells in a culture).

#### Predictive Medicine

[00229] The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual.

[00230] Generally, the invention provides, a method of determining if a subject is at risk for a disorder related to a lesion in or the misexpression of a gene which encodes 57242.

[00231] Such disorders include, e.g., a disorder associated with the misexpression of 57242, or lipid metabolism related disorder.

[00232] The method includes one or more of the following:

detecting, in a tissue of the subject, the presence or absence of a mutation which affects the expression of the 57242 gene, or detecting the presence or absence of a mutation in a region which controls the expression of the gene, e.g., a mutation in the 5' control region;

detecting, in a tissue of the subject, the presence or absence of a mutation which alters the structure of the 57242 gene;

detecting, in a tissue of the subject, the misexpression of the 57242 gene, at the mRNA level, e.g., detecting a non-wild type level of a mRNA ;

detecting, in a tissue of the subject, the misexpression of the gene, at the protein level, e.g., detecting a non-wild type level of a 57242 polypeptide.

[00233] In preferred embodiments the method includes: ascertaining the existence of at least one of: a deletion of one or more nucleotides from the 57242 gene; an insertion of one or more nucleotides into the gene, a point mutation, e.g., a substitution of one or more nucleotides of the gene, a gross chromosomal rearrangement of the gene, e.g., a translocation, inversion, or deletion.

[00234] For example, detecting the genetic lesion can include: (i) providing a probe/primer including an oligonucleotide containing a region of nucleotide sequence which hybridizes to a sense or antisense sequence from SEQ ID NO:1 naturally occurring mutants thereof or 5' or 3' flanking sequences naturally associated with the 57242 gene; (ii) exposing the probe/primer to nucleic acid of the tissue; and detecting, by hybridization, e.g., *in situ* hybridization, of the probe/primer to the nucleic acid, the presence or absence of the genetic lesion.

[00235] In preferred embodiments detecting the misexpression includes ascertaining the existence of at least one of: an alteration in the level of a messenger RNA transcript of the 57242 gene; the presence of a non-wild type splicing pattern of a messenger RNA transcript of the gene; or a non-wild type level of 57242.

[00236] Methods of the invention can be used prenatally or to determine if a subject's offspring will be at risk for a disorder.

[00237] In preferred embodiments the method includes determining the structure of a 57242 gene, an abnormal structure being indicative of risk for the disorder.

[00238] In preferred embodiments the method includes contacting a sample from the subject with an antibody to the 57242 protein or a nucleic acid, which hybridizes specifically with the gene. These and other embodiments are discussed below.

Diagnostic and Prognostic Assays

[00239] The presence, level, or absence of 57242 protein or nucleic acid in a biological sample can be evaluated by obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting 57242 protein or nucleic acid (e.g., mRNA, genomic DNA) that encodes 57242 protein such that the presence of 57242 protein or nucleic acid is detected in the biological sample. The term "biological sample" includes tissues, cells and biological fluids isolated from a subject, as well as tissues, cells and fluids present within a subject. A preferred biological sample is serum. The level of expression of the 57242 gene can be measured in a number of ways, including, but not limited to: measuring the mRNA encoded by the 57242 genes; measuring the amount of protein encoded by the 57242 genes; or measuring the activity of the protein encoded by the 57242 genes.

[00240] The level of mRNA corresponding to the 57242 gene in a cell can be determined both by *in situ* and by *in vitro* formats.

[00241] The isolated mRNA can be used in hybridization or amplification assays that include, but are not limited to, Southern or Northern analyses, polymerase chain reaction analyses and probe arrays. One preferred diagnostic method for the detection of mRNA levels involves contacting the isolated mRNA with a nucleic acid molecule (probe) that can hybridize to the mRNA encoded by the gene being detected. The nucleic acid probe can be, for example, a full-length 57242 nucleic acid, such as the nucleic acid of SEQ ID NO:1 or SEQ ID NO:3, or a portion thereof, such as an oligonucleotide of at least 7, 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to 57242 mRNA or genomic DNA. Other suitable probes for use in the diagnostic assays are described herein.

[00242] In one format, mRNA (or cDNA) is immobilized on a surface and contacted with the probes, for example by running the isolated mRNA on an agarose gel and transferring the mRNA from the gel to a membrane, such as nitrocellulose. In an alternative format, the

probes are immobilized on a surface and the mRNA (or cDNA) is contacted with the probes, for example, in a two-dimensional gene chip array. A skilled artisan can adapt known mRNA detection methods for use in detecting the level of mRNA encoded by the 57242 genes.

[00243] The level of mRNA in a sample that is encoded by one of 57242 can be evaluated with nucleic acid amplification, e.g., by rtPCR (Mullis, 1987, U.S. Patent No. 4,683,202), ligase chain reaction (Barany, 1991, *Proc. Natl. Acad. Sci. USA* 88:189-193), self sustained sequence replication (Guatelli et al., 1990, *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh et al., 1989, *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi et al., 1988, *Bio/Technology* 6:1197), rolling circle replication (Lizardi et al., U.S. Patent No. 5,854,033) or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques known in the art. As used herein, amplification primers are defined as being a pair of nucleic acid molecules that can anneal to 5' or 3' regions of a gene (plus and minus strands, respectively, or vice-versa) and contain a short region in between. In general, amplification primers are from about 10 to 30 nucleotides in length and flank a region from about 50 to 200 nucleotides in length. Under appropriate conditions and with appropriate reagents, such primers permit the amplification of a nucleic acid molecule comprising the nucleotide sequence flanked by the primers.

[00244] For *in situ* methods, a cell or tissue sample can be prepared/processed and immobilized on a support, typically a glass slide, and then contacted with a probe that can hybridize to mRNA that encodes the 57242 gene being analyzed.

[00245] In another embodiment, the methods further contacting a control sample with a compound or agent capable of detecting 57242 mRNA, or genomic DNA, and comparing the presence of 57242 mRNA or genomic DNA in the control sample with the presence of 57242 mRNA or genomic DNA in the test sample.

[00246] A variety of methods can be used to determine the level of protein encoded by 57242. In general, these methods include contacting an agent that selectively binds to the protein, such as an antibody with a sample, to evaluate the level of protein in the sample. In a preferred embodiment, the antibody bears a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (e.g., Fab or F(ab')<sub>2</sub>) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (i.e., physically

linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with a detectable substance. Examples of detectable substances are provided herein.

[00247] The detection methods can be used to detect 57242 protein in a biological sample *in vitro* as well as *in vivo*. *In vitro* techniques for detection of 57242 protein include enzyme linked immunosorbent assays (ELISAs), immunoprecipitations, immunofluorescence, enzyme immunoassay (EIA), radioimmunoassay (RIA), and Western blot analysis. *In vivo* techniques for detection of 57242 protein include introducing into a subject a labeled anti-57242 antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

[00248] In another embodiment, the methods further include contacting the control sample with a compound or agent capable of detecting 57242 protein, and comparing the presence of 57242 protein in the control sample with the presence of 57242 protein in the test sample.

[00249] The invention also includes kits for detecting the presence of 57242 in a biological sample. For example, the kit can include a compound or agent capable of detecting 57242 protein or mRNA in a biological sample; and a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect 57242 protein or nucleic acid.

[00250] For antibody-based kits, the kit can include: (1) a first antibody (e.g., attached to a solid support) which binds to a polypeptide corresponding to a marker of the invention; and, optionally, (2) a second, different antibody which binds to either the polypeptide or the first antibody and is conjugated to a detectable agent.

[00251] For oligonucleotide-based kits, the kit can include: (1) an oligonucleotide, e.g., a detectably labeled oligonucleotide, which hybridizes to a nucleic acid sequence encoding a polypeptide corresponding to a marker of the invention or (2) a pair of primers useful for amplifying a nucleic acid molecule corresponding to a marker of the invention. The kit can also include a buffering agent, a preservative, or a protein-stabilizing agent. The kit can also include components necessary for detecting the detectable agent (e.g., an enzyme or a substrate). The kit can also contain a control sample or a series of control samples which can be assayed and compared to the test sample contained. Each component of the kit can be enclosed within an individual container and all of the various containers can be within a

single package, along with instructions for interpreting the results of the assays performed using the kit.

[00252] The diagnostic methods described herein can identify subjects having, or at risk of developing, a disease or disorder associated with misexpressed or aberrant or unwanted 57242 expression or activity. As used herein, the term "unwanted" includes an unwanted phenomenon involved in a biological response such as pain or deregulated cell proliferation.

[00253] In one embodiment, a disease or disorder associated with aberrant or unwanted 57242 expression or activity is identified. A test sample is obtained from a subject and 57242 protein or nucleic acid (e.g., mRNA or genomic DNA) is evaluated, wherein the level, e.g., the presence or absence, of 57242 protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant or unwanted 57242 expression or activity. As used herein, a "test sample" refers to a biological sample obtained from a subject of interest, including a biological fluid (e.g., serum), cell sample, or tissue.

[00254] The prognostic assays described herein can be used to determine whether a subject can be administered an agent (e.g., an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder associated with aberrant or unwanted 57242 expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a cellular growth related disorder.

[00255] The methods of the invention can also be used to detect genetic alterations in a 57242 gene, thereby determining if a subject with the altered gene is at risk for a disorder characterized by misregulation in 57242 protein activity or nucleic acid expression, such as a cellular growth related disorder. In preferred embodiments, the methods include detecting, in a sample from the subject, the presence or absence of a genetic alteration characterized by at least one of an alteration affecting the integrity of a gene encoding a 57242-protein, or the mis-expression of the 57242 gene. For example, such genetic alterations can be detected by ascertaining the existence of at least one of 1) a deletion of one or more nucleotides from a 57242 gene; 2) an addition of one or more nucleotides to a 57242 gene; 3) a substitution of one or more nucleotides of a 57242 gene, 4) a chromosomal rearrangement of a 57242 gene; 5) an alteration in the level of a messenger RNA transcript of a 57242 gene, 6) aberrant modification of a 57242 gene, such as of the methylation pattern of the genomic DNA, 7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a 57242

gene, 8) a non-wild type level of a 57242-protein, 9) allelic loss of a 57242 gene, and 10) inappropriate post-translational modification of a 57242-protein.

[00256] An alteration can be detected without a probe/primer in a polymerase chain reaction, such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR), the latter of which can be particularly useful for detecting point mutations in the 57242-gene. This method can include the steps of collecting a sample of cells from a subject, isolating nucleic acid (e.g., genomic, mRNA or both) from the sample, contacting the nucleic acid sample with one or more primers which specifically hybridize to a 57242 gene under conditions such that hybridization and amplification of the 57242-gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

[00257] Alternative amplification methods include: self sustained sequence replication (Guatelli, J.C. et al., (1990) *Proc. Natl. Acad. Sci. USA* 87:1874-1878), transcriptional amplification system (Kwoh, D.Y. et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:1173-1177), Q-Beta Replicase (Lizardi, P.M. et al., (1988) *Bio-Technology* 6:1197), or other nucleic acid amplification methods, followed by the detection of the amplified molecules using techniques known to those of skill in the art.

[00258] In another embodiment, mutations in a 57242 gene from a sample cell can be identified by detecting alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined, e.g., by gel electrophoresis and compared. Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Patent No. 5,498,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

[00259] In other embodiments, genetic mutations in 57242 can be identified by hybridizing a sample and control nucleic acids, e.g., DNA or RNA, two-dimensional arrays, e.g., chip based arrays. Such arrays include a plurality of addresses, each of which is positionally distinguishable from the other. A different probe is located at each address of the plurality. The arrays can have a high density of addresses, e.g., can contain hundreds or thousands of oligonucleotides probes (Cronin, M.T. et al., (1996) *Human Mutation* 7: 244-

255; Kozal, M.J. et al., (1996) *Nature Medicine* 2:753-759). For example, genetic mutations in 57242 can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin, M.T. et al., *supra*. Briefly, a first hybridization array of probes can be used to scan through long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one complementary to the wild-type gene and the other complementary to the mutant gene.

[00260] In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the 57242 gene and detect mutations by comparing the sequence of the sample 57242 with the corresponding wild-type (control) sequence.

Automated sequencing procedures can be utilized when performing the diagnostic assays ((1995) *Biotechniques* 19:448), including sequencing by mass spectrometry.

[00261] Other methods for detecting mutations in the 57242 gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA heteroduplexes (Myers et al., (1985) *Science* 230:1242; Cotton et al., (1988) *Proc. Natl. Acad. Sci. USA* 85:4397; Saleeba et al., (1992) *Methods Enzymol.* 217:286-295).

[00262] In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in 57242 cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu et al., (1994) *Carcinogenesis* 15:1657-1662; U.S. Patent No. 5,459,039).

[00263] In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in 57242 genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita et al., (1989) *Proc. Natl. Acad. Sci. USA*: 86:2766, see also Cotton, (1993) *Mutat. Res.* 285:125-144; and Hayashi, (1992) *Genet. Anal. Tech. Appl.* 9:73-79). Single-stranded DNA fragments of sample and control 57242 nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic

acids varies according to sequence, the resulting alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA (rather than DNA), in which the secondary structure is more sensitive to a change in sequence. In a preferred embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility (Keen et al., (1991) *Trends Genet.* 7:5).

[00264] In yet another embodiment, the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE) (Myers et al., (1985) *Nature* 313:495). When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA (Rosenbaum and Reissner, (1987) *Biophys. Chem.* 26:12753).

[00265] Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension (Saiki et al., (1986) *Nature* 324:163); Saiki et al., (1989) *Proc. Natl. Acad. Sci. USA* 86:6230).

[00266] Alternatively, allele specific amplification technology which depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs et al., (1989) *Nucleic Acids Res.* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner, (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection (Gasparini et al., (1992) *Mol. Cell Probes* 6:1). It is anticipated that in certain embodiments amplification may also be performed using Taq ligase for amplification (Barany, (1991) *Proc. Natl. Acad. Sci USA* 88:189). In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

[00267] The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a 57242 gene.

Use of 57242 Molecules as Surrogate Markers

[00268] The 57242 molecules of the invention are also useful as markers of disorders or disease states, as markers for precursors of disease states, as markers for predisposition of disease states, as markers of drug activity, or as markers of the pharmacogenomic profile of a subject. Using the methods described herein, the presence, absence and/or quantity of the 57242 molecules of the invention may be detected, and may be correlated with one or more biological states *in vivo*. For example, the 57242 molecules of the invention may serve as surrogate markers for one or more disorders or disease states or for conditions leading up to disease states. As used herein, a "surrogate marker" is an objective biochemical marker which correlates with the absence or presence of a disease or disorder, or with the progression of a disease or disorder (*e.g.*, with the presence or absence of a tumor). The presence or quantity of such markers is independent of the disease. Therefore, these markers may serve to indicate whether a particular course of treatment is effective in lessening a disease state or disorder. Surrogate markers are of particular use when the presence or extent of a disease state or disorder is difficult to assess through standard methodologies (*e.g.*, early stage tumors), or when an assessment of disease progression is desired before a potentially dangerous clinical endpoint is reached (*e.g.*, an assessment of cardiovascular disease may be made using cholesterol levels as a surrogate marker, and an analysis of HIV infection may be made using HIV RNA levels as a surrogate marker, well in advance of the undesirable clinical outcomes of myocardial infarction or fully-developed AIDS). Examples of the use of surrogate markers in the art include: Koomen *et al.* (2000) *J. Mass. Spectrom.* 35: 258-264; and James (1994) *AIDS Treatment News Archive* 209.

[00269] The 57242 molecules of the invention are also useful as pharmacodynamic markers. As used herein, a "pharmacodynamic marker" is an objective biochemical marker which correlates specifically with drug effects. The presence or quantity of a pharmacodynamic marker is not related to the disease state or disorder for which the drug is being administered; therefore, the presence or quantity of the marker is indicative of the

presence or activity of the drug in a subject. For example, a pharmacodynamic marker may be indicative of the concentration of the drug in a biological tissue, in that the marker is either expressed or transcribed or not expressed or transcribed in that tissue in relationship to the level of the drug. In this fashion, the distribution or uptake of the drug may be monitored by the pharmacodynamic marker. Similarly, the presence or quantity of the pharmacodynamic marker may be related to the presence or quantity of the metabolic product of a drug, such that the presence or quantity of the marker is indicative of the relative breakdown rate of the drug *in vivo*. Pharmacodynamic markers are of particular use in increasing the sensitivity of detection of drug effects, particularly when the drug is administered in low doses. Since even a small amount of a drug may be sufficient to activate multiple rounds of marker (e.g., a 57242 marker) transcription or expression, the amplified marker may be in a quantity which is more readily detectable than the drug itself. Also, the marker may be more easily detected due to the nature of the marker itself; for example, using the methods described herein, anti-57242 antibodies may be employed in an immune-based detection system for a 57242 protein marker, or 57242-specific radiolabeled probes may be used to detect a 57242 mRNA marker. Furthermore, the use of a pharmacodynamic marker may offer mechanism-based prediction of risk due to drug treatment beyond the range of possible direct observations. Examples of the use of pharmacodynamic markers in the art include: Matsuda *et al.* US 6,033,862; Hattis *et al.* (1991) *Env. Health Perspect.* 90: 229-238; Schentag (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S21-S24; and Nicolau (1999) *Am. J. Health-Syst. Pharm.* 56 Suppl. 3: S16-S20.

[00270] The 57242 molecules of the invention are also useful as pharmacogenomic markers. As used herein, a "pharmacogenomic marker" is an objective biochemical marker which correlates with a specific clinical drug response or susceptibility in a subject (see, e.g., McLeod *et al.* (1999) *Eur. J. Cancer* 35(12): 1650-1652). The presence or quantity of the pharmacogenomic marker is related to the predicted response of the subject to a specific drug or class of drugs prior to administration of the drug. By assessing the presence or quantity of one or more pharmacogenomic markers in a subject, a drug therapy which is most appropriate for the subject, or which is predicted to have a greater degree of success, may be selected. For example, based on the presence or quantity of RNA, or protein (e.g., 57242 protein or RNA) for specific tumor markers in a subject, a drug or course of treatment may be selected that is optimized for the treatment of the specific tumor likely to be present in the subject. Similarly, the presence or absence of a specific sequence mutation

in 57242 DNA may correlate 57242 drug response. The use of pharmacogenomic markers therefore permits the application of the most appropriate treatment for each subject without having to administer the therapy.

#### Pharmaceutical Compositions

[00271] The nucleic acid and polypeptides, fragments thereof, as well as anti-57242 antibodies (also referred to herein as "active compounds") of the invention can be incorporated into pharmaceutical compositions. Such compositions typically include the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein the language "pharmaceutically acceptable carrier" includes solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Supplementary active compounds can also be incorporated into the compositions.

[00272] A pharmaceutical composition is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates and agents for the adjustment of tonicity such as sodium chloride or dextrose. pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

[00273] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the

contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

[00274] Sterile injectable solutions can be prepared by incorporating the active compound in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle which contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[00275] Oral compositions generally include an inert diluent or an edible carrier. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules, e.g., gelatin capsules. Oral compositions can also be prepared using a fluid carrier for use as a mouthwash. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

[00276] For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, e.g., a gas such as carbon dioxide, or a nebulizer.

[00277] Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

[00278] The compounds can also be prepared in the form of suppositories (e.g., with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

[00279] In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Patent No. 4,522,811.

[00280] It is advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier.

[00281] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and

therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>. Compounds which exhibit high therapeutic indices are preferred. While compounds that exhibit toxic side effects may be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00282] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage may vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose may be formulated in animal models to achieve a circulating plasma concentration range that includes the IC<sub>50</sub> (i.e., the concentration of the test compound which achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma may be measured, for example, by high performance liquid chromatography.

[00283] As defined herein, a therapeutically effective amount of protein or polypeptide (i.e., an effective dosage) ranges from about 0.001 to 30 mg/kg body weight, preferably about 0.01 to 25 mg/kg body weight, more preferably about 0.1 to 20 mg/kg body weight, and even more preferably about 1 to 10 mg/kg, 2 to 9 mg/kg, 3 to 8 mg/kg, 4 to 7 mg/kg, or 5 to 6 mg/kg body weight. The protein or polypeptide can be administered one time per week for between about 1 to 10 weeks, preferably between 2 to 8 weeks, more preferably between about 3 to 7 weeks, and even more preferably for about 4, 5, or 6 weeks. The skilled artisan will appreciate that certain factors may influence the dosage and timing required to effectively treat a subject, including but not limited to the severity of the disease or disorder, previous treatments, the general health and/or age of the subject, and other diseases present. Moreover, treatment of a subject with a therapeutically effective amount of a protein, polypeptide, or antibody can include a single treatment or, preferably, can include a series of treatments.

[00284] For antibodies, the preferred dosage is 0.1 mg/kg of body weight (generally 10 mg/kg to 20 mg/kg). If the antibody is to act in the brain, a dosage of 50 mg/kg to 100 mg/kg is usually appropriate. Generally, partially human antibodies and fully human antibodies have a longer half-life within the human body than other antibodies.

Accordingly, lower dosages and less frequent administration is often possible.

Modifications such as lipidation can be used to stabilize antibodies and to enhance uptake and tissue penetration (e.g., into the brain). A method for lipidation of antibodies is described by Cruikshank et al., ((1997) *J. Acquired Immune Deficiency Syndromes and Human Retrovirology* 14:193).

[00285] The present invention encompasses agents which modulate expression or activity. An agent may, for example, be a small molecule. For example, such small molecules include, but are not limited to, peptides, peptidomimetics (e.g., peptoids), amino acids, amino acid analogs, polynucleotides, polynucleotide analogs, nucleotides, nucleotide analogs, organic or inorganic compounds (i.e., including heteroorganic and organometallic compounds) having a molecular weight less than about 10,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 5,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 1,000 grams per mole, organic or inorganic compounds having a molecular weight less than about 500 grams per mole, and salts, esters, and other pharmaceutically acceptable forms of such compounds.

[00286] Exemplary doses include milligram or microgram amounts of the small molecule per kilogram of subject or sample weight (e.g., about 1 microgram per kilogram to about 500 milligrams per kilogram, about 100 micrograms per kilogram to about 5 milligrams per kilogram, or about 1 microgram per kilogram to about 50 micrograms per kilogram. It is furthermore understood that appropriate doses of a small molecule depend upon the potency of the small molecule with respect to the expression or activity to be modulated. When one or more of these small molecules is to be administered to an animal (e.g., a human) in order to modulate expression or activity of a polypeptide or nucleic acid of the invention, a physician, veterinarian, or researcher may, for example, prescribe a relatively low dose at first, subsequently increasing the dose until an appropriate response is obtained. In addition, it is understood that the specific dose level for any particular animal subject will depend upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, gender, and diet of the subject, the time of administration, the route of administration, the rate of excretion, any drug combination, and the degree of expression or activity to be modulated.

[00287] An antibody (or fragment thereof) may be conjugated to a therapeutic moiety such as a cytotoxin, a therapeutic agent or a radioactive metal ion. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include taxol, cytochalasin

B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

[00288] The conjugates of the invention can be used for modifying a given biological response, the drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria toxin; a protein such as tumor necrosis factor, .alpha.-interferon, .beta.-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

[00289] Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980.

[00290] The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by, for example, intravenous injection, local administration (see U.S. Patent 5,328,470) or by stereotactic injection (see e.g., Chen et al., (1994) *Proc. Natl. Acad. Sci. USA* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, e.g., retroviral vectors, the pharmaceutical preparation can include one or more cells which produce the gene delivery system.

[00291] The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Methods of Treatment:

[00292] The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant or unwanted 57242 expression or activity. With regards to both prophylactic and therapeutic methods of treatment, such treatments may be specifically tailored or modified, based on knowledge obtained from the field of pharmacogenomics. "Pharmacogenomics", as used herein, refers to the application of genomics technologies such as gene sequencing, statistical genetics, and gene expression analysis to drugs in clinical development and on the market. More specifically, the term refers the study of how a patient's genes determine his or her response to a drug (e.g., a patient's "drug response phenotype", or "drug response genotype".) Thus, another aspect of the invention provides methods for tailoring an individual's prophylactic or therapeutic treatment with either the 57242 molecules of the present invention or 57242 modulators according to that individual's drug response genotype. Pharmacogenomics allows a clinician or physician to target prophylactic or therapeutic treatments to patients who will most benefit from the treatment and to avoid treatment of patients who will experience toxic drug-related side effects.

[00293] In one aspect, the invention provides a method for preventing in a subject, a disease or condition associated with an aberrant or unwanted 57242 expression or activity, by administering to the subject a 57242 or an agent which modulates 57242 expression or at least one 57242 activity. Subjects at risk for a disease which is caused or contributed to by aberrant or unwanted 57242 expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the 57242 aberrance, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of 57242 aberrance, for example, a 57242, 57242 agonist or 57242 antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

[00294] It is possible that some 57242 disorders can be caused, at least in part, by an abnormal level of gene product, or by the presence of a gene product exhibiting abnormal

activity. As such, the reduction in the level and/or activity of such gene products would bring about the amelioration of disorder symptoms.

[00295] As discussed, successful treatment of 57242 disorders can be brought about by techniques that serve to inhibit the expression or activity of target gene products. For example, compounds, e.g., an agent identified using an assays described above, that proves to exhibit negative modulatory activity, can be used in accordance with the invention to prevent and/or ameliorate symptoms of 57242 disorders. Such molecules can include, but are not limited to peptides, phosphopeptides, small organic or inorganic molecules, or antibodies (including, for example, polyclonal, monoclonal, humanized, anti-idiotypic, chimeric or single chain antibodies, and FAb, F(ab')<sub>2</sub> and FAb expression library fragments, scFV molecules, and epitope-binding fragments thereof).

[00296] Further, antisense and ribozyme molecules that inhibit expression of the target gene can also be used in accordance with the invention to reduce the level of target gene expression, thus effectively reducing the level of target gene activity. Still further, triple helix molecules can be utilized in reducing the level of target gene activity. Antisense, ribozyme and triple helix molecules are discussed above.

[00297] It is possible that the use of antisense, ribozyme, and/or triple helix molecules to reduce or inhibit mutant gene expression can also reduce or inhibit the transcription (triple helix) and/or translation (antisense, ribozyme) of mRNA produced by normal target gene alleles, such that the concentration of normal target gene product present can be lower than is necessary for a normal phenotype. In such cases, nucleic acid molecules that encode and express target gene polypeptides exhibiting normal target gene activity can be introduced into cells via gene therapy method. Alternatively, in instances in that the target gene encodes an extracellular protein, it can be preferable to co-administer normal target gene protein into the cell or tissue in order to maintain the requisite level of cellular or tissue target gene activity.

[00298] Another method by which nucleic acid molecules may be utilized in treating or preventing a disease characterized by 57242 expression is through the use of aptamer molecules specific for 57242 protein. Aptamers are nucleic acid molecules having a tertiary structure which permits them to specifically bind to protein ligands (see, e.g., Osborne, et al., *Curr. Opin. Chem. Biol.* 1997, 1(1): 5-9; and Patel, D.J., *Curr. Opin. Chem. Biol.* 1997 Jun; 1(1):32-46). Since nucleic acid molecules may in many cases be more conveniently introduced into target cells than therapeutic protein molecules may be, aptamers offer a

method by which 57242 protein activity may be specifically decreased without the introduction of drugs or other molecules which may have pluripotent effects.

[00299] Antibodies can be generated that are both specific for target gene product and that reduce target gene product activity. Such antibodies may, therefore, be administered in instances whereby negative modulatory techniques are appropriate for the treatment of 57242 disorders. For a description of antibodies, see the Antibody section above.

[00300] In circumstances wherein injection of an animal or a human subject with a 57242 protein or epitope for stimulating antibody production is harmful to the subject, it is possible to generate an immune response against 57242 through the use of anti-idiotypic antibodies (see, for example, Herlyn, D., *Ann. Med.* 1999;31(1):66-78; and Bhattacharya-Chatterjee, M., and Foon, K.A., *Cancer Treat. Res.* 1998;94:51-68). If an anti-idiotypic antibody is introduced into a mammal or human subject, it should stimulate the production of anti-anti-idiotypic antibodies, which should be specific to the 57242 protein. Vaccines directed to a disease characterized by 57242 expression may also be generated in this fashion.

[00301] In instances where the target antigen is intracellular and whole antibodies are used, internalizing antibodies may be preferred. Lipofectin or liposomes can be used to deliver the antibody or a fragment of the Fab region that binds to the target antigen into cells. Where fragments of the antibody are used, the smallest inhibitory fragment that binds to the target antigen is preferred. For example, peptides having an amino acid sequence corresponding to the Fv region of the antibody can be used. Alternatively, single chain neutralizing antibodies that bind to intracellular target antigens can also be administered. Such single chain antibodies can be administered, for example, by expressing nucleotide sequences encoding single-chain antibodies within the target cell population (see e.g., Marasco et al., (1993, *Proc. Natl. Acad. Sci. USA* 90:7889-7893).

[00302] The identified compounds that inhibit target gene expression, synthesis and/or activity can be administered to a patient at therapeutically effective doses to prevent, treat or ameliorate 57242 disorders. A therapeutically effective dose refers to that amount of the compound sufficient to result in amelioration of symptoms of the disorders.

[00303] Toxicity and therapeutic efficacy of such compounds can be determined by standard pharmaceutical procedures in cell cultures or experimental animals, e.g., for determining the LD<sub>50</sub> (the dose lethal to 50% of the population) and the ED<sub>50</sub> (the dose therapeutically effective in 50% of the population). The dose ratio between toxic and therapeutic effects is the therapeutic index and it can be expressed as the ratio LD<sub>50</sub>/ED<sub>50</sub>.

Compounds that exhibit large therapeutic indices are preferred. While compounds that exhibit toxic side effects can be used, care should be taken to design a delivery system that targets such compounds to the site of affected tissue in order to minimize potential damage to uninfected cells and, thereby, reduce side effects.

[00304] The data obtained from the cell culture assays and animal studies can be used in formulating a range of dosage for use in humans. The dosage of such compounds lies preferably within a range of circulating concentrations that include the ED<sub>50</sub> with little or no toxicity. The dosage can vary within this range depending upon the dosage form employed and the route of administration utilized. For any compound used in the method of the invention, the therapeutically effective dose can be estimated initially from cell culture assays. A dose can be formulated in animal models to achieve a circulating plasma concentration range that includes the IC<sub>50</sub> (i.e., the concentration of the test compound that achieves a half-maximal inhibition of symptoms) as determined in cell culture. Such information can be used to more accurately determine useful doses in humans. Levels in plasma can be measured, for example, by high performance liquid chromatography.

[00305] Another example of determination of effective dose for an individual is the ability to directly assay levels of "free" and "bound" compound in the serum of the test subject. Such assays may utilize antibody mimics and/or "biosensors" that have been created through molecular imprinting techniques. The compound which is able to modulate 57242 activity is used as a template, or "imprinting molecule", to spatially organize polymerizable monomers prior to their polymerization with catalytic reagents. The subsequent removal of the imprinted molecule leaves a polymer matrix which contains a repeated "negative image" of the compound and is able to selectively rebind the molecule under biological assay conditions. A detailed review of this technique can be seen in Ansell, R. J. et al., (1996) *Current Opinion in Biotechnology* 7:89-94 and in Shea, K.J., (1994) *Trends in Polymer Science* 2:166-173. Such "imprinted" affinity matrixes are amenable to ligand-binding assays, whereby the immobilized monoclonal antibody component is replaced by an appropriately imprinted matrix. An example of the use of such matrixes in this way can be seen in Vlatakis, G. et al., (1993) *Nature* 361:645-647. Through the use of isotope-labeling, the "free" concentration of compound which modulates the expression or activity of 57242 can be readily monitored and used in calculations of IC<sub>50</sub>.

[00306] Such "imprinted" affinity matrixes can also be designed to include fluorescent groups whose photon-emitting properties measurably change upon local and selective

binding of target compound. These changes can be readily assayed in real time using appropriate fiberoptic devices, in turn allowing the dose in a test subject to be quickly optimized based on its individual IC<sub>50</sub>. A rudimentary example of such a "biosensor" is discussed in Kriz, D. et al., (1995) *Analytical Chemistry* 67:2142-2144.

[00307] Another aspect of the invention pertains to methods of modulating 57242 expression or activity for therapeutic purposes. Accordingly, in an exemplary embodiment, the modulatory method of the invention involves contacting a cell with a 57242 or agent that modulates one or more of the activities of 57242 protein activity associated with the cell. An agent that modulates 57242 protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring target molecule of a 57242 protein (e.g., a 57242 substrate or receptor), a 57242 antibody, a 57242 agonist or antagonist, a peptidomimetic of a 57242 agonist or antagonist, or other small molecule.

[00308] In one embodiment, the agent stimulates one or 57242 activities. Examples of such stimulatory agents include active 57242 protein and a nucleic acid molecule encoding 57242. In another embodiment, the agent inhibits one or more 57242 activities. Examples of such inhibitory agents include antisense 57242 nucleic acid molecules, anti-57242 antibodies, and 57242 inhibitors. These modulatory methods can be performed *in vitro* (e.g., by culturing the cell with the agent) or, alternatively, *in vivo* (e.g., by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant or unwanted expression or activity of a 57242 protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (e.g., an agent identified by a screening assay described herein), or combination of agents that modulates (e.g., upregulates or downregulates) 57242 expression or activity. In another embodiment, the method involves administering a 57242 protein or nucleic acid molecule as therapy to compensate for reduced, aberrant, or unwanted 57242 expression or activity.

[00309] Stimulation of 57242 activity is desirable in situations in which 57242 is abnormally downregulated and/or in which increased 57242 activity is likely to have a beneficial effect. For example, stimulation of 57242 activity is desirable in situations in which a 57242 is downregulated and/or in which increased 57242 activity is likely to have a beneficial effect. Likewise, inhibition of 57242 activity is desirable in situations in which 57242 is abnormally upregulated and/or in which decreased 57242 activity is likely to have a beneficial effect.

[00310] The 57242 molecules can act as novel diagnostic targets and therapeutic agents for controlling one or more of cellular proliferative and/or differentiative disorders, cardiovascular disorders, as described above, as well as disorders associated with metabolism or bone metabolism, hematopoietic disorders, liver disorders, viral diseases, or pain disorders.

[00311] Diseases of metabolic imbalance include, but are not limited to, obesity, anorexia nervosa, cachexia, lipid disorders including hyperlipidemia, and diabetes.

[00312] Aberrant expression and/or activity of 57242 molecules may mediate disorders associated with bone metabolism. "Bone metabolism" refers to direct or indirect effects in the formation or degeneration of bone structures, e.g., bone formation, bone resorption, etc., which may ultimately affect the concentrations in serum of calcium and phosphate. This term also includes activities and effects in bone cells, e.g. osteoclasts and osteoblasts, mediated by 57242 molecules that may in turn result in bone formation and degeneration.

For example, 57242 molecules may support different activities of bone resorbing osteoclasts such as the stimulation of differentiation of monocytes and mononuclear phagocytes into osteoclasts. Accordingly, 57242 molecules that modulate the production of bone cells can influence bone formation and degeneration, and thus may be used to treat bone disorders. Examples of such disorders include, but are not limited to, osteoporosis, osteodystrophy, osteomalacia, rickets, osteitis fibrosa cystica, renal osteodystrophy, osteosclerosis, anti-convulsant treatment, osteopenia, fibrogenesis-imperfecta ossium, secondary hyperparathyroidism, hypoparathyroidism, hyperparathyroidism, cirrhosis, obstructive jaundice, drug induced metabolism, medullary carcinoma, chronic renal disease, rickets, sarcoidosis, glucocorticoid antagonism, malabsorption syndrome, steatorrhea, tropical sprue, idiopathic hypercalcemia and milk fever.

[00313] Normal bone homeostatic mechanisms require the balanced activity of cells of the bone forming (osteoblast) and bone resorbing (osteoclast) lineage. Inappropriate regulation of either process can lead to a decrease in bone mass and the subsequent development of osteoporosis. Mesenchymal stem cell precursors residing in the bone marrow are able to differentiate into multiple cell lineages depending upon environmental cues present in the bone marrow space. Included among these differentiation lineages are the mature fat-cell (the white adipocyte) and the mature bone forming cell (the osteoblast). Therapeutic intervention that could increase the number of osteoblasts generated in the bone marrow, via the manipulation of the differentiation capacity of the mesenchymal precursor

pool, is one means to increase bone strength. More specifically, if the precursors in the marrow that are normally targeted for adipocyte development could be therapeutically blocked, default programming of the mesenchymal precursors could result in the differentiation of this precursor pool toward the osteoblast lineage. The increased numbers of osteoblasts would therefore be capable of increasing bone mass and strength. 57242 is strongly induced during adipocyte differentiation (see Examples). Antagonism of this 57242 may block adipocyte differentiation *in vivo*. As a consequence, precursors will be available to differentiate, either by default or via environmental cues residing within the marrow space, to differentiate into an osteogenic lineage. The result will be an increase in mature bone forming osteoblasts.

[00314] Examples of hematopoietic disorders include, but are not limited to, autoimmune diseases (including, for example, diabetes mellitus, arthritis (including rheumatoid arthritis, juvenile rheumatoid arthritis, osteoarthritis, psoriatic arthritis), multiple sclerosis, encephalomyelitis, myasthenia gravis, systemic lupus erythematosus, autoimmune thyroiditis, dermatitis (including atopic dermatitis and eczematous dermatitis), psoriasis, Sjögren's Syndrome, Crohn's disease, aphthous ulcer, iritis, conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma, allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis, proctitis, drug eruptions, leprosy reversal reactions, erythema nodosum leprosum, autoimmune uveitis, allergic encephalomyelitis, acute necrotizing hemorrhagic encephalopathy, idiopathic bilateral progressive sensorineural hearing loss, aplastic anemia, pure red cell anemia, idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis, chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue, lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis, uveitis posterior, and interstitial lung fibrosis), graft-versus-host disease, cases of transplantation, and allergy such as, atopic allergy.

[00315] Disorders which may be treated or diagnosed by methods described herein include, but are not limited to, disorders associated with an accumulation in the liver of fibrous tissue, such as that resulting from an imbalance between production and degradation of the extracellular matrix accompanied by the collapse and condensation of preexisting fibers. The methods described herein can be used to diagnose or treat hepatocellular necrosis or injury induced by a wide variety of agents including processes which disturb homeostasis, such as an inflammatory process, tissue damage resulting from toxic injury or altered hepatic blood flow, and infections (e.g., bacterial, viral and parasitic). For example,

the methods can be used for the early detection of hepatic injury, such as portal hypertension or hepatic fibrosis. In addition, the methods can be employed to detect liver fibrosis attributed to inborn errors of metabolism, for example, fibrosis resulting from a storage disorder such as Gaucher's disease (lipid abnormalities) or a glycogen storage disease,  $\text{A1-antitrypsin}$  deficiency; a disorder mediating the accumulation (e.g., storage) of an exogenous substance, for example, hemochromatosis (iron-overload syndrome) and copper storage diseases (Wilson's disease), disorders resulting in the accumulation of a toxic metabolite (e.g., tyrosinemia, fructosuria and galactosemia) and peroxisomal disorders (e.g., Zellweger syndrome). Additionally, the methods described herein may be useful for the early detection and treatment of liver injury associated with the administration of various chemicals or drugs, such as for example, methotrexate, isoniazid, oxyphenisatin, methyldopa, chlorpromazine, tolbutamide or alcohol, or which represents a hepatic manifestation of a vascular disorder such as obstruction of either the intrahepatic or extrahepatic bile flow or an alteration in hepatic circulation resulting, for example, from chronic heart failure, veno-occlusive disease, portal vein thrombosis or Budd-Chiari syndrome.

**[00316]** Additionally, 57242 molecules may play an important role in the etiology of certain viral diseases, including but not limited to, Hepatitis B, Hepatitis C and Herpes Simplex Virus (HSV). Modulators of 57242 activity could be used to control viral diseases. The modulators can be used in the treatment and/or diagnosis of viral infected tissue or virus-associated tissue fibrosis, especially liver and liver fibrosis. Also, 57242 modulators can be used in the treatment and/or diagnosis of virus-associated carcinoma, especially hepatocellular cancer.

**[00317]** Disorders involving the brain include, but are not limited to, disorders involving neurons, and disorders involving glia, such as astrocytes, oligodendrocytes, ependymal cells, and microglia; cerebral edema, raised intracranial pressure and herniation, and hydrocephalus; malformations and developmental diseases, such as neural tube defects, forebrain anomalies, posterior fossa anomalies, and syringomyelia and hydromyelia; perinatal brain injury; cerebrovascular diseases, such as those related to hypoxia, ischemia, and infarction, including hypotension, hypoperfusion, and low-flow states--global cerebral ischemia and focal cerebral ischemia--infarction from obstruction of local blood supply, intracranial hemorrhage, including intracerebral (intraparenchymal) hemorrhage, subarachnoid hemorrhage and ruptured berry aneurysms, and vascular malformations, hypertensive cerebrovascular disease, including lacunar infarcts, slit hemorrhages, and

hypertensive encephalopathy; infections, such as acute meningitis, including acute pyogenic (bacterial) meningitis and acute aseptic (viral) meningitis, acute focal suppurative infections, including brain abscess, subdural empyema, and extradural abscess, chronic bacterial meningoencephalitis, including tuberculosis and mycobacterioses, neurosyphilis, and neuroborreliosis (Lyme disease), viral meningoencephalitis, including arthropod-borne (Arbo) viral encephalitis, *Herpes simplex* virus Type 1, *Herpes simplex* virus Type 2, *Varicella-zoster* virus (*Herpes zoster*), cytomegalovirus, poliomyelitis, rabies, and human immunodeficiency virus 1, including HIV-1 meningoencephalitis (subacute encephalitis), vacuolar myopathy, AIDS-associated myopathy, peripheral neuropathy, and AIDS in children, progressive multifocal leukoencephalopathy, subacute sclerosing panencephalitis, fungal meningoencephalitis, other infectious diseases of the nervous system; transmissible spongiform encephalopathies (prion diseases); demyelinating diseases, including multiple sclerosis, multiple sclerosis variants, acute disseminated encephalomyelitis and acute necrotizing hemorrhagic encephalomyelitis, and other diseases with demyelination; degenerative diseases, such as degenerative diseases affecting the cerebral cortex, including Alzheimer disease and Pick disease, degenerative diseases of basal ganglia and brain stem, including Parkinsonism, idiopathic Parkinson disease (paralysis agitans), progressive supranuclear palsy, corticobasal degeneration, multiple system atrophy, including striatonigral degeneration, Shy-Drager syndrome, and olivopontocerebellar atrophy, and Huntington disease; spinocerebellar degenerations, including spinocerebellar ataxias, including Friedreich ataxia, and ataxia-telangiectasia, degenerative diseases affecting motor neurons, including amyotrophic lateral sclerosis (motor neuron disease), bulbospinal atrophy (Kennedy syndrome), and spinal muscular atrophy; inborn errors of metabolism, such as leukodystrophies, including Krabbe disease, metachromatic leukodystrophy, adrenoleukodystrophy, Pelizaeus-Merzbacher disease, and Canavan disease, mitochondrial encephalomyopathies, including Leigh disease and other mitochondrial encephalomyopathies; toxic and acquired metabolic diseases, including vitamin deficiencies such as thiamine (vitamin B<sub>1</sub>) deficiency and vitamin B<sub>12</sub> deficiency, neurologic sequelae of metabolic disturbances, including hypoglycemia, hyperglycemia, and hepatic encephalopathy, toxic disorders, including carbon monoxide, methanol, ethanol, and radiation, including combined methotrexate and radiation-induced injury; tumors, such as gliomas, including astrocytoma, including fibrillary (diffuse) astrocytoma and glioblastoma multiforme, pilocytic astrocytoma, pleomorphic xanthoastrocytoma, and brain stem glioma,

oligodendrolioma, and ependymoma and related paraventricular mass lesions, neuronal tumors, poorly differentiated neoplasms, including medulloblastoma, other parenchymal tumors, including primary brain lymphoma, germ cell tumors, and pineal parenchymal tumors, meningiomas, metastatic tumors, paraneoplastic syndromes, peripheral nerve sheath tumors, including schwannoma, neurofibroma, and malignant peripheral nerve sheath tumor (malignant schwannoma), and neurocutaneous syndromes (phakomatoses), including neurofibromatosis, including Type 1 neurofibromatosis (NF1) and TYPE 2 neurofibromatosis (NF2), tuberous sclerosis, and Von Hippel-Lindau disease.

**[00318]** Disorders involving the heart, include but are not limited to, heart failure, including but not limited to, cardiac hypertrophy, left-sided heart failure, and right-sided heart failure; ischemic heart disease, including but not limited to angina pectoris, myocardial infarction, chronic ischemic heart disease, and sudden cardiac death; hypertensive heart disease, including but not limited to, systemic (left-sided) hypertensive heart disease and pulmonary (right-sided) hypertensive heart disease; valvular heart disease, including but not limited to, valvular degeneration caused by calcification, such as calcific aortic stenosis, calcification of a congenitally bicuspid aortic valve, and mitral annular calcification, and myxomatous degeneration of the mitral valve (mitral valve prolapse), rheumatic fever and rheumatic heart disease, infective endocarditis, and noninfected vegetations, such as nonbacterial thrombotic endocarditis and endocarditis of systemic lupus erythematosus (Libman-Sacks disease), carcinoid heart disease, and complications of artificial valves; myocardial disease, including but not limited to dilated cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, and myocarditis; pericardial disease, including but not limited to, pericardial effusion and hemopericardium and pericarditis, including acute pericarditis and healed pericarditis, and rheumatoid heart disease; neoplastic heart disease, including but not limited to, primary cardiac tumors, such as myxoma, lipoma, papillary fibroelastoma, rhabdomyoma, and sarcoma, and cardiac effects of noncardiac neoplasms; congenital heart disease, including but not limited to, left-to-right shunts—late cyanosis, such as atrial septal defect, ventricular septal defect, patent ductus arteriosus, and atrioventricular septal defect, right-to-left shunts—early cyanosis, such as tetralogy of fallot, transposition of great arteries, truncus arteriosus, tricuspid atresia, and total anomalous pulmonary venous connection, obstructive congenital anomalies, such as coarctation of aorta, pulmonary stenosis and atresia, and aortic stenosis and atresia, and disorders involving cardiac transplantation.

[00319] Disorders involving blood vessels include, but are not limited to, responses of vascular cell walls to injury, such as endothelial dysfunction and endothelial activation and intimal thickening; vascular diseases including, but not limited to, congenital anomalies, such as arteriovenous fistula, atherosclerosis, and hypertensive vascular disease, such as hypertension; inflammatory disease—the vasculitides, such as giant cell (temporal) arteritis, Takayasu arteritis, polyarteritis nodosa (classic), Kawasaki syndrome (mucocutaneous lymph node syndrome), microscopic polyangiitis (microscopic polyarteritis, hypersensitivity or leukocytoclastic angiitis), Wegener granulomatosis, thromboangiitis obliterans (Buerger disease), vasculitis associated with other disorders, and infectious arteritis; Raynaud disease; aneurysms and dissection, such as abdominal aortic aneurysms, syphilitic (luetic) aneurysms, and aortic dissection (dissecting hematoma); disorders of veins and lymphatics, such as varicose veins, thrombophlebitis and phlebothrombosis, obstruction of superior vena cava (superior vena cava syndrome), obstruction of inferior vena cava (inferior vena cava syndrome), and lymphangitis and lymphedema; tumors, including benign tumors and tumor-like conditions, such as hemangioma, lymphangioma, glomus tumor (glomangioma), vascular ectasias, and bacillary angiomatosis, and intermediate-grade (borderline low-grade malignant) tumors, such as Kaposi sarcoma and hemangioendothelioma, and malignant tumors, such as angiosarcoma and hemangiopericytoma; and pathology of therapeutic interventions in vascular disease, such as balloon angioplasty and related techniques and vascular replacement, such as coronary artery bypass graft surgery.

[00320] Additionally, 57242 may play an important role in the regulation of pain disorders. Examples of pain disorders include, but are not limited to, pain response elicited during various forms of tissue injury, e.g., inflammation, infection, and ischemia, usually referred to as hyperalgesia (described in, for example, Fields, H.L., (1987) *Pain*, New York:McGraw-Hill); pain associated with musculoskeletal disorders, e.g., joint pain; tooth pain; headaches; pain associated with surgery; pain related to irritable bowel syndrome; or chest pain.

#### Pharmacogenomics

[00321] The 57242 molecules of the present invention, as well as agents, or modulators which have a stimulatory or inhibitory effect on 57242 activity (e.g., 57242 gene expression) as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) 57242 associated disorders (e.g.,

cellular growth related disorders) associated with aberrant or unwanted 57242 activity. In conjunction with such treatment, pharmacogenomics (i.e., the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) may be considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, a physician or clinician may consider applying knowledge obtained in relevant pharmacogenomics studies in determining whether to administer a 57242 molecule or 57242 modulator as well as tailoring the dosage and/or therapeutic regimen of treatment with a 57242 molecule or 57242 modulator.

[00322] Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See, for example, Eichelbaum, M. et al. (1996) *Clin. Exp. Pharmacol. Physiol.* 23(10-11):983-985 and Linder, M.W. et al. (1997) *Clin. Chem.* 43(2):254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare genetic defects or as naturally-occurring polymorphisms. For example, glucose-6-phosphate dehydrogenase deficiency (G6PD) is a common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

[00323] One pharmacogenomics approach to identifying genes that predict drug response, known as "a genome-wide association", relies primarily on a high-resolution map of the human genome consisting of already known gene-related markers (e.g., a "bi-allelic" gene marker map which consists of 60,000-100,000 polymorphic or variable sites on the human genome, each of which has two variants.) Such a high-resolution genetic map can be compared to a map of the genome of each of a statistically significant number of patients taking part in a Phase II/III drug trial to identify markers associated with a particular observed drug response or side effect. Alternatively, such a high-resolution map can be generated from a combination of some ten million known single nucleotide polymorphisms (SNPs) in the human genome. As used herein, a "SNP" is a common alteration that occurs in a single nucleotide base in a stretch of DNA. For example, a SNP may occur once per every 1000 bases of DNA. A SNP may be involved in a disease process, however, the vast

majority may not be disease-associated. Given a genetic map based on the occurrence of such SNPs, individuals can be grouped into genetic categories depending on a particular pattern of SNPs in their individual genome. In such a manner, treatment regimens can be tailored to groups of genetically similar individuals, taking into account traits that may be common among such genetically similar individuals.

[00324] Alternatively, a method termed the "candidate gene approach", can be utilized to identify genes that predict drug response. According to this method, if a gene that encodes a drug's target is known (e.g., a 57242 protein of the present invention), all common variants of that gene can be fairly easily identified in the population and it can be determined if having one version of the gene versus another is associated with a particular drug response.

[00325] Alternatively, a method termed the "gene expression profiling", can be utilized to identify genes that predict drug response. For example, the gene expression of an animal dosed with a drug (e.g., a 57242 molecule or 57242 modulator of the present invention) can give an indication whether gene pathways related to toxicity have been turned on.

[00326] Information generated from more than one of the above pharmacogenomics approaches can be used to determine appropriate dosage and treatment regimens for prophylactic or therapeutic treatment of an individual. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus enhance therapeutic or prophylactic efficiency when treating a subject with a 57242 molecule or 57242 modulator, such as a modulator identified by one of the exemplary screening assays described herein.

[00327] The present invention further provides methods for identifying new agents, or combinations, that are based on identifying agents that modulate the activity of one or more of the gene products encoded by one or more of the 57242 genes of the present invention, wherein these products may be associated with resistance of the cells to a therapeutic agent. Specifically, the activity of the proteins encoded by the 57242 genes of the present invention can be used as a basis for identifying agents for overcoming agent resistance. By blocking the activity of one or more of the resistance proteins, target cells, e.g., cancer cells, will become sensitive to treatment with an agent that the unmodified target cells were resistant to.

[00328] Monitoring the influence of agents (e.g., drugs) on the expression or activity of a 57242 protein can be applied in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase 57242 gene expression,

protein levels, or upregulate 57242 activity, can be monitored in clinical trials of subjects exhibiting decreased 57242 gene expression, protein levels, or downregulated 57242 activity. Alternatively, the effectiveness of an agent determined by a screening assay to decrease 57242 gene expression, protein levels, or downregulate 57242 activity, can be monitored in clinical trials of subjects exhibiting increased 57242 gene expression, protein levels, or upregulated 57242 activity. In such clinical trials, the expression or activity of a 57242 gene, and preferably, other genes that have been implicated in, for example, a 57242-associated disorder can be used as a "read out" or markers of the phenotype of a particular cell.

#### Other Embodiments

[00329] In another aspect, the invention features, a method of analyzing a plurality of capture probes. The method can be used, e.g., to analyze gene expression. The method includes: providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., a nucleic acid or peptide sequence; contacting the array with a 57242, preferably purified, nucleic acid, preferably purified, polypeptide, preferably purified, or antibody, and thereby evaluating the plurality of capture probes. Binding, e.g., in the case of a nucleic acid, hybridization with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the 57242 nucleic acid, polypeptide, or antibody.

[00330] The capture probes can be a set of nucleic acids from a selected sample, e.g., a sample of nucleic acids derived from a control or non-stimulated tissue or cell.

[00331] The method can include contacting the 57242 nucleic acid, polypeptide, or antibody with a first array having a plurality of capture probes and a second array having a different plurality of capture probes. The results of each hybridization can be compared, e.g., to analyze differences in expression between a first and second sample. The first plurality of capture probes can be from a control sample, e.g., a wild type, normal, or non-diseased, non-stimulated, sample, e.g., a biological fluid, tissue, or cell sample. The second plurality of capture probes can be from an experimental sample, e.g., a mutant type, at risk, disease-state or disorder-state, or stimulated, sample, e.g., a biological fluid, tissue, or cell sample.

[00332] The plurality of capture probes can be a plurality of nucleic acid probes each of which specifically hybridizes, with an allele of 57242. Such methods can be used to diagnose a subject, e.g., to evaluate risk for a disease or disorder, to evaluate suitability of a selected treatment for a subject, to evaluate whether a subject has a disease or disorder. 57242 is associated with G protein-coupled receptor activity, thus it is useful for disorders associated with abnormal lipid metabolism.

[00333] The method can be used to detect SNPs, as described above.

[00334] In another aspect, the invention features, a method of analyzing a plurality of probes. The method is useful, e.g., for analyzing gene expression. The method includes: providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which express or mis express 57242 or from a cell or subject in which a 57242 mediated response has been elicited, e.g., by contact of the cell with 57242 nucleic acid or protein, or administration to the cell or subject 57242 nucleic acid or protein; contacting the array with one or more inquiry probe, wherein an inquiry probe can be a nucleic acid, polypeptide, or antibody (which is preferably other than 57242 nucleic acid, polypeptide, or antibody); providing a two dimensional array having a plurality of addresses, each address of the plurality being positionally distinguishable from each other address of the plurality, and each address of the plurality having a unique capture probe, e.g., wherein the capture probes are from a cell or subject which does not express 57242 (or does not express as highly as in the case of the 57242 positive plurality of capture probes) or from a cell or subject which in which a 57242 mediated response has not been elicited (or has been elicited to a lesser extent than in the first sample); contacting the array with one or more inquiry probes (which is preferably other than a 57242 nucleic acid, polypeptide, or antibody), and thereby evaluating the plurality of capture probes. Binding, e.g., in the case of a nucleic acid, hybridization with a capture probe at an address of the plurality, is detected, e.g., by signal generated from a label attached to the nucleic acid, polypeptide, or antibody.

[00335] In another aspect, the invention features, a method of analyzing 57242, e.g., analyzing structure, function, or relatedness to other nucleic acid or amino acid sequences. The method includes: providing a 57242 nucleic acid or amino acid sequence; comparing the 57242 sequence with one or more preferably a plurality of sequences from a collection of sequences, e.g., a nucleic acid or protein sequence database; to thereby analyze 57242.

[00336] Preferred databases include GenBank™. The method can include evaluating the sequence identity between a 57242 sequence and a database sequence. The method can be performed by accessing the database at a second site, e.g., over the internet.

[00337] In another aspect, the invention features, a set of oligonucleotides, useful, e.g., for identifying SNP's, or identifying specific alleles of 57242. The set includes a plurality of oligonucleotides, each of which has a different nucleotide at an interrogation position, e.g., an SNP or the site of a mutation. In a preferred embodiment, the oligonucleotides of the plurality identical in sequence with one another (except for differences in length). The oligonucleotides can be provided with different labels, such that an oligonucleotides which hybridizes to one allele provides a signal that is distinguishable from an oligonucleotides which hybridizes to a second allele.

[00338] This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patents and published patent applications cited throughout this application are incorporated herein by reference.

## EXAMPLES

### Example 1: Identification and Characterization of Human 57242 cDNAs

[00339] The human 57242 sequence (SEQ ID NO:1), which is approximately 1475 nucleotides long including untranslated regions, contains a predicted methionine-initiated coding sequence of about 1041 nucleotides (nucleotides 154-1194 of SEQ ID NO:1; SEQ ID NO:3). The coding sequence encodes a 346 amino acid protein (SEQ ID NO:2).

### Example 2: 57242 Gene Expression in Human and Mouse Tissues

[00340] Tissues were collected from 7 week old male C57/Bl6J mice fed ad libitum, from 6 week old male C57/Bl6J mice housed at either 4°C or room temperature for different times prior to tissue collection or from 10 week old ob/ob or wt control male mice. Human bone marrow derived mesenchymal stem cells were purchased from Cambrex Inc. Human RNA was purchased from Zen-Bio (adipose tissue and adipocyte samples), Clontech, or was prepared from samples available at Millennium. 3T3-L1 cells and HiB-1B cells were differentiated in vitro using established protocols (Puigserver et al., Cell 92:829-839 (1998), Wu et al., J Clin Invest 101:22-32 (1998)). RNA was prepared using the trizol method and treated with DNase to remove contaminating genomic DNA. cDNA was synthesized using random hexamer primers. Mock cDNA synthesis in the absence of reverse transcriptase

resulted in samples with no detectable PCR amplification of the control 18S gene confirming efficient removal of genomic DNA contamination. Taqman analysis was performed following the manufacturer's directions.

[00341] PCR probes were designed by PrimerExpress software (PE Biosystems) based on the respective sequences of murine and human 57242. The following probes and primers were used:

m57242 forward primer: 5' GGCAGCAGCTGACCAGACA 3' (SEQ ID NO:4)

m57242 reverse primer: 5' GAACACAGAAGCCACCACCAT 3' (SEQ ID NO:5)

m57242 probe: 5' ATGAGGAGGGCCACCCGGITCAT 3' (SEQ ID NO:6)

h57242 forward primer: 5' TGCAGTCTGAAACCCAAGCA 3' (SEQ ID NO:7)

h57242 reverse primer: 5' TGCGACCGAGGTTCGAA 3' (SEQ ID NO:8)

h57242 probe: 5' CACAAAGGCCGGAAGAGATGCCA 3' (SEQ ID NO:9)

[00342] To allow standardization between different tissues, each sample contained two probes distinguished by different fluorescent labels, a probe for the gene of interest (e.g. 57242) as well as a probe for 18S RNA as an internal control. The threshold values at which the PCR amplification started were determined using the manufacturer's software.

[00343] The following method was used to quantitatively calculate 57242 gene expression in the tissue samples, relative to the 18S RNA expression in the same tissue. The threshold values at which the PCR amplification started were determined using the manufacturer's software. PCR cycle number at threshold value was designated as CT. Relative expression was calculated as  $2^{((CT_{\text{test}}-CT_{18S}) \text{ tissue of interest} - (CT_{\text{test}}-CT_{18S}) \text{ lowest expressing tissue in panel})}$ . Samples were run in duplicate and the averages of 2 relative expression levels that were linear to the amount of template cDNA with a slope similar to the slope for the internal control 18S were used.

**TABLE 2: 57242 Expression in Normal Tissues**

Human Tissue	Rel. Expr.	Human Tissue	Rel. Expr.	Mouse Tissue	Rel. Expr.
Artery	0.0042	Heart	9.805	Brain	26.9190
Vein	0.0044	Skeletal Muscle	4.418	Hypothalamus	24.8471
Heart	0.0052	Kidney	44.53	Bat	3136.65
Skeletal Muscle	0.0022	Primary	337.5	Wat	3304.32213
		Adipocyte			
Kidney	0.0941	Preadipocyte	5.58	Heart	9.9370
Adipose	0.3453	Brain	49.2	Muscle	52.3508
Breast	0.3477	Liver	9	Small intestine	90.8375
Pancreas	0.0071	Spleen	29	Small intestine	101.1472
			2		
Skin	0.0152			Spleen	28.0682
Brain-Cortex	0.0037			Kidney	210.1212
Hypothalamus	0.0029			Lung	67.1883
Nerve	0.0037			Liver	1.0070
Ovary	0.0088				
Prostate	0.0666				
Salivary Gland	0.0455				
Colon	0				
Small Intestine	0				
Lung	0.0245				
Liver	0				
Spleen	0.0621				
Lymph Node	0.0099				

[00344] The results of expression of 57242 in human tissues by Taqman analysis showed highest levels of expression of 57242 in subcutaneous adipose tissue and breast, with lower expression in kidney, prostate and spleen (Table 2). 57242 mRNA was present in primary human adipocytes, but was absent from preadipocytes (Table 2), demonstrating that the signal in fat is due to expression in adipocytes rather than other cell types.

[00345] TaqMan analysis was also performed in mouse tissues as indicated above. The mouse orthologue of 57242 was highly expressed in both brown and white adipose tissue, but was present at considerably lower levels in all other tissues tested (Table 2).

EXAMPLE 3: Regulation of 57242 Expression

[00346] To determine whether 57242 expression is regulated under conditions that affect adipocyte differentiation or brown or white adipocyte metabolism, expression of 57242 was measured in cells or tissues of mice exposed to various conditions. For analyses, TaqMan analysis was performed as indicated above.

Regulation of 57242 under conditions promoting cell differentiation

Primary human esenchymal stem cell differentiation

[00347] Regulation of the transcript encoding 57242 in human bone marrow derived mesenchymal stem cells was evaluated in cells cultured under conditions that promote differentiation of cells to either mature adipocytes or mature osteoblasts. To induce adipogenesis, cells were cultured to 100% confluency in standard growth medium containing 10% fetal calf serum. The medium was then replaced with adipogenesis induction medium (DMEM-high glucose supplemented with 1.0  $\mu$ M dexamethasone, 0.2 mM indomethacin, 0.01 mg/ml insulin, 0.5 mM 3-isobutyl-1-methyl-xanthine, 10% fetal bovine serum and 0.05 units/ml penicillin and 0.05  $\mu$ g streptomycin). The cells were kept in the adipogenesis induction medium for three days and then switched to adipogenesis maintenance medium (DMEM-high glucose supplemented with 10 % fetal bovine serum, 0.01 mg/ml insulin and 0.05 units/ml penicillin and 0.05  $\mu$ g streptomycin) for an additional three days. This pattern of growth in adipogenesis inducing and adipogenesis maintenance medium was repeated a total of three times followed by an additional 4 days in adipogenic maintenance medium. The cells were then either directly harvested for RNA extraction or fixed in 10% buffered formalin and stained with Oil Red "O" to detect adipogenic differentiation. To induce the mesenchymal stem cells to the osteoblast lineage, the precursor cells were plated in standard growth medium and when the cells reached approximately 80% confluence, the growth medium was replaced with osteogenesis induction medium (0.01  $\mu$ M dexamethasone, 0.05mM ascorbic acid-2-phosphate and 10 mM  $\beta$ -glycerophosphate). The cells were then cultured for a period of 17 days with a medium change (osteogenic induction medium) every fourth day. Cells were

either directly harvested for RNA extraction or monitored for bone nodule formation by staining with Alizarin Red

[00348] As illustrated in Table 3, 57242 was expressed at low levels in the mesenchymal precursor stem cell population but was highly induced during adipogenic differentiation. In contrast, there was a small induction of 57242 early in the switch to osteogenic differentiation medium but levels were subsequently reduced during the latter stages of osteogenesis.

**TABLE 3: Regulation of 57242 Expression During Human Mesenchymal Stem Cell Differentiation**

Time	Rel. Expr. Adipocyte	Rel. Expr. Osteoblast
Day 0	1.0	1.0
Day 3	4.52	1.35
Day 10	7.25	0.72
Day 17/20	6.89	0.58

#### 3T3-L1 cell differentiation

[00349] We also tested expression of 57242 during differentiation of the mouse preadipocyte cell line 3T3-L1. L1 preadipocytes were grown in 10% Calf serum. When the cells reached confluence, they were induced to differentiate in the medium containing 10  $\mu$ g/ml insulin, 0.5 mM isobutyl-methylxanthine, 1  $\mu$ M Dexamethasone and 10% FBS in DMEM. Forty-eight hours post-induction, cells were maintained in 10% FBS in DMEM with 2.5  $\mu$ g/ml insulin.

[00350] 57242 was expressed at very low levels in preadipocytes and was dramatically upregulated during adipocyte differentiation, consistent with expression of 57242 in adipocytes rather than other cell types in the adipose tissue (see Table 4).

**TABLE 4: Regulation of 57242 Expression During Mouse 3T3-L1 Differentiation**

Time	Rel. Expr. Adipocyte
Day 0	1.06644194
Day 10	417.147841

Regulation under conditions of increased thermogenesis

[00351] Activation of a GPCR-mediated signaling pathway often results in downregulation of transcription of the GPCR itself. For example, activation of thermogenesis *in vivo* by noradrenaline or *in vitro* by beta3-adrenergic agonists or cAMP causes downregulation of the beta3-adrenergic receptor (Onai et al., Am J Physiol 269:R519-526, (1995), Grannemann et al., Am J Physiol 268:C1040-1044 (1995), Klaus et al., Mol Cell Endocrinol 109:189-195 (1995)). Exposure of mice to the cold, a treatment known to increase thermogenesis, showed that 57242 expression is decreased in WAT, and even more pronounced in BAT (see Table 4).

[00352] H1B preadipocytes grown in 10% FBS in DMEM were induced to differentiate in medium containing 20  $\mu$ M insulin, 0.5 mM isobutyl-methylxanthine, 1  $\mu$ M Dexamethasone, 1nM T3, 0.125 mM indomethacin and 10% FBS (heat inactivated) in DMEM. Forty-eight hours post-induction, cells were maintained in 10% FBS (heat inactivated) in DMEM with 20  $\mu$ g and 1nM T3. Differentiated H1B cells (day 2, 4 and 5) stimulated with 1 mM 8-bromo-cyclic AMP for 6 hr. also demonstrated decreased 57242 expression (see Table 6).

TABLE 5 Regulation of 57242 Expression in Adipose

Tissue During Cold Exposure

WAT		BAT	
Treatment	Rel. Expr.	Treatment	Rel. Expr.
0h	26.4619814	0h	15.9139155
3h	14.2458976	3h	7.50030154
12h	18.0707927	12h	1.06252924
24h	14.3031064	24h	1.98362392

TABLE 6 Regulation of 57242

Expression in adipose tissue

in response to cAMP

Treatment	Rel. Expr.
d3 control	3.00096088
d3 cAMP	1.02485834
d4 control	5.81714753
d4 cAMP	1.3805246

Regulation of 57242 in genetically obese mice

[00353] To determine whether GPCR57242 is regulated in obese, insulin-resistant mice, we examined expression in genetically obese ob/ob mice. 57242 expression was considerably lower in ob/ob mice compared to wild-type control mice (Table 7).

TABLE 7 57242

## Expression in ob/ob Mice

Genotype	Rel. Expr.
wt WAT	4.925050867
ob/ob WAT	1.00697974

Regulation of 57242 during fasting and refeeding

[00354] Stimulation of lipolysis is believed to be an effective strategy for decreasing body weight. To examine a possible role of 57242 in lipolysis we examined its expression in white and brown adipose tissues of mice which had been fasted for 3 days. Under those conditions, lipolysis is maximally stimulated and mice rely on fatty acids released from adipose tissue as an energy source. Fasting mice for 3 days decreased 57242 expression in both white and brown adipose tissue. Refeeding for 1 and 2 days caused a small increase compared to fasted animals (Table 8).

TABLE 8 Regulation of 57242 Expression in Adipose

## Tissue During Starvation and Refeeding

WAT		BAT	
Treatment	Rel. Expr.	Treatment	Rel. Expr.
Day 0	7.0948993	Day 0	7.31925873
Day 3	1.67053695	Day 3	1.00697974
Day 3+1	2.258050854	Day 3+1	2.631796851
Day 3+2	4.171465885	Day 3+2	2.085732942

Example 4: Recombinant Expression of 57242 in Bacterial Cells

[00355] For expression of recombinant 57242, a glutathione-S-transferase (GST) fusion polypeptide of 57242 is expressed in *E. coli*, isolated and characterized. Specifically, 57242 is genetically fused to GST and this fusion polypeptide is expressed in *E. coli*, e.g., strain PEB199. Expression of the GST-57242 fusion protein in PEB199 is induced with IPTG. The recombinant fusion polypeptide is purified from crude bacterial lysates of the induced PEB199 strain by affinity chromatography on glutathione beads. Using polyacrylamide gel electrophoretic analysis of the polypeptide purified from the bacterial lysates, the molecular weight of the resultant fusion polypeptide is determined.

Example 5: Expression of Recombinant 57242 Protein in mammalian Cells

[00356] To express the 57242 gene in mammalian cells, for example COS cells, the pcDNA/Amp vector by Invitrogen Corporation (San Diego, CA) is used. This vector contains an SV40 origin of replication, an ampicillin resistance gene, an *E. coli* replication origin, a CMV promoter followed by a polylinker region, and an SV40 intron and polyadenylation site. A DNA fragment encoding the entire 57242 protein and an HA tag (Wilson et al. (1984) *Cell* 37:767) or a FLAG tag fused in-frame to its 3' end of the fragment is cloned into the polylinker region of the vector, thereby placing the expression of the recombinant protein under the control of the CMV promoter.

[00357] To construct the plasmid, the 57242 DNA sequence is amplified by PCR using two primers. The 5' primer contains the restriction site of interest followed by approximately twenty nucleotides of the 57242 coding sequence starting from the initiation codon; the 3' end sequence contains complementary sequences to the other restriction site of interest, a translation stop codon, the HA tag or FLAG tag and the last 20 nucleotides of the 57242 coding sequence. The PCR amplified fragment and the pCDNA/Amp vector are digested with the appropriate restriction enzymes and the vector is dephosphorylated using the CIAP enzyme (New England Biolabs, Beverly, MA). Preferably the two restriction sites chosen are different so that the 57242 gene is inserted in the correct orientation. The ligation mixture is transformed into *E. coli* cells (strains HB101, DH5 $\square$ , SURE, available from Stratagene Cloning Systems, La Jolla, CA, can be used), the transformed culture is plated on ampicillin media plates, and resistant colonies are selected. Plasmid DNA is isolated from transformants and examined by restriction analysis for the presence of the correct fragment.

[00358] COS cells are subsequently transfected with the 57242-pcDNA/Amp plasmid DNA using the calcium phosphate or calcium chloride co-precipitation methods, DEAE-dextran-mediated transfection, lipofection, or electroporation. Other suitable methods for transfecting host cells can be found in Sambrook, J., Fritsh, E. F., and Maniatis, T.

*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.* The expression of the 57242 polypeptide is detected by radiolabelling ( $^{35}\text{S}$ -methionine or  $^{35}\text{S}$ -cysteine available from NEN, Boston, MA, can be used) and immunoprecipitation (Harlow, E. and Lane, D. *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1988) using an HA specific monoclonal antibody. Briefly, the cells are labeled for 8 hours with  $^{35}\text{S}$ -methionine (or  $^{35}\text{S}$ -cysteine). The culture media are then collected and the cells are lysed using detergents (RIPA buffer, 150 mM NaCl, 1% NP-40, 0.1% SDS, 0.5% DOC, 50 mM Tris, pH 7.5). Both the cell lysate and the culture media are precipitated with an HA specific monoclonal antibody. Precipitated polypeptides are then analyzed by SDS-PAGE.

[00359] Alternatively, DNA containing the 57242 coding sequence is cloned directly into the polylinker of the pCDNA/Amp vector using the appropriate restriction sites. The resulting plasmid is transfected into COS cells in the manner described above, and the expression of the 57242 polypeptide is detected by radiolabelling and immunoprecipitation using a 57242 specific monoclonal antibody.

#### Equivalents

[00360] Those skilled in the art will recognize, or be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed is:

1. An isolated nucleic acid molecule selected from the group consisting of:
  - a) a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3;
  - b) a nucleic acid molecule comprising a fragment of at least 300 nucleotides of the nucleotide sequence of SEQ ID NO:1 or SEQ ID NO:3;
  - c) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
  - d) a nucleic acid molecule which encodes a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2; and
  - e) a nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof, under stringent conditions.
2. The isolated nucleic acid molecule of claim 1, which is selected from the group consisting of:
  - a) a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, and
  - b) a nucleic acid molecule which encodes a polypeptide comprising the amino acid sequence of SEQ ID NO:2.
3. The nucleic acid molecule of claim 1 further comprising vector nucleic acid sequences.
4. The nucleic acid molecule of claim 1 further comprising nucleic acid sequences encoding a heterologous polypeptide.
5. A host cell which contains the nucleic acid molecule of claim 1.
6. The host cell of claim 5 which is a mammalian host cell.

7. A non-human mammalian host cell containing the nucleic acid molecule of claim 1.

8. An isolated polypeptide selected from the group consisting of:

- a) a polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 60% identical to a nucleic acid comprising the nucleotide sequence of SEQ ID NO:1, SEQ ID NO:3, or a complement thereof;
- b) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3, or a complement thereof under stringent conditions; and
- c) a fragment of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2.

9. The isolated polypeptide of claim 8 comprising the amino acid sequence of SEQ ID NO:2.

10. The polypeptide of claim 8 further comprising heterologous amino acid sequences.

11. An antibody which selectively binds to a polypeptide of claim 8.

12. A method for producing a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- b) a polypeptide comprising a fragment of the amino acid sequence of SEQ ID NO:2, wherein the fragment comprises at least 15 contiguous amino acids of SEQ ID NO:2; and
- c) a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a nucleic acid molecule comprising SEQ ID NO:1, SEQ ID NO:3;

comprising culturing the host cell of claim 5 under conditions in which the nucleic acid molecule is expressed.

13. A method for detecting the presence of a polypeptide of claim 8 in a sample, comprising:

- a) contacting the sample with a compound which selectively binds to a polypeptide of claim 8; and
- b) determining whether the compound binds to the polypeptide in the sample.

14. The method of claim 13, wherein the compound which binds to the polypeptide is an antibody.

15. A kit comprising a compound which selectively binds to a polypeptide of claim 8 and instructions for use.

16. A method for detecting the presence of a nucleic acid molecule of claim 1 in a sample, comprising the steps of:

- a) contacting the sample with a nucleic acid probe or primer which selectively hybridizes to the nucleic acid molecule; and
- b) determining whether the nucleic acid probe or primer binds to a nucleic acid molecule in the sample.

17. The method of claim 16, wherein the sample comprises mRNA molecules and is contacted with a nucleic acid probe.

18. A kit comprising a compound which selectively hybridizes to a nucleic acid molecule of claim 1 and instructions for use.

19. A method for identifying a compound which binds to a polypeptide of claim 8 comprising the steps of:

- a) contacting a polypeptide, or a cell expressing a polypeptide of claim 8 with a test compound; and
- b) determining whether the polypeptide binds to the test compound.

20. The method of claim 19, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) detection of binding by direct detecting of test compound/polypeptide binding;
- b) detection of binding using a competition binding assay;
- c) detection of binding using an assay for 43238-mediated signal transduction..

21. A method for modulating the activity of a polypeptide of claim 8 comprising contacting a polypeptide or a cell expressing a polypeptide of claim 8 with a compound which binds to the polypeptide in a sufficient concentration to modulate the activity of the polypeptide.

22. A method for identifying a compound which modulates the activity of a polypeptide of claim 8, comprising:

- a) contacting a polypeptide of claim 8 with a test compound; and
- b) determining the effect of the test compound on the activity of the polypeptide to thereby identify a compound which modulates the activity of the polypeptide.

23. A method of identifying a nucleic acid molecule associated with a metabolic disorder comprising:

- a) contacting a sample comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3; and
- b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a nucleic acid molecule associated with a metabolic disorder.

24. The method of claim 23, wherein said hybridization probe is detectably labeled.

25. The method of claim 23, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

26. The method of claim 23, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

27. The method of claim 23, wherein said detecting is by *in situ* hybridization.

28. A method of identifying a nucleic acid associated with a metabolic disorder comprising:

- a) contacting a sample comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or 3;
- b) incubating said sample under conditions that allow nucleic acid amplification; and
- c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a nucleic acid molecule associated with a metabolic disorder.

29. The method of claim 6, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

30. The method of any one of claims 23 or 28, wherein said method is used to detect mRNA in said sample.

31. The method of any one of claims 23 or 28, wherein said method is used to detect genomic DNA in said sample.

32. A method of identifying a polypeptide associated with a metabolic disorder comprising:

- a) contacting a sample comprising polypeptides with a 57242 binding substance; and
- b) detecting the presence of a polypeptide in said sample that binds to said 57242 binding substance, thereby identifying a polypeptide associated with a metabolic disorder.

33. The method of claim 32, wherein said binding substance is an antibody.

34. The method of claim 32, wherein said binding substance is detectably labeled.

35. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a hybridization probe comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3; and

b) detecting the presence of a nucleic acid molecule in said sample that hybridizes to said probe, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

36. The method of claim 35, wherein said hybridization probe is detectably labeled.

37. The method of claim 35, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and southern blotting prior to contacting with said hybridization probe.

38. The method of claim 35, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis and northern blotting prior to contacting with said hybridization probe.

39. The method of claim 35, wherein said detecting is by *in situ* hybridization.

40. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising nucleic acid molecules with a first and a second amplification primer, said first primer comprising at least 25 contiguous nucleotides of SEQ ID NO:1 or 3 and said second primer comprising at least 25 contiguous nucleotides from the complement of SEQ ID NO:1 or 3;

b) incubating said sample under conditions that allow nucleic acid amplification; and

c) detecting the presence of a nucleic acid molecule in said sample that is amplified, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

41. The method of claim 40, wherein said sample comprising nucleic acid molecules is subjected to agarose gel electrophoresis after said incubation step.

42. The method of any one of claims 35 or 40, wherein said method is used to detect mRNA in said sample.

43. The method of any one of claims 35 or 40, wherein said method is used to detect genomic DNA in said sample.

44. A method of identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder comprising:

a) contacting a sample obtained from said subject comprising polypeptides with a 57242 binding substance; and

b) detecting the presence of a polypeptide in said sample that binds to said 57242 binding substance, thereby identifying a subject having a metabolic disorder, or at risk for developing a metabolic disorder.

45. The method of claim 44, wherein said binding substance is an antibody.

46. The method of claim 44, wherein said binding substance is detectably labeled.

47. A method for identifying a compound capable of treating a metabolic disorder characterized by aberrant 57242 nucleic acid expression or 57242 polypeptide activity comprising assaying the ability of the compound to modulate 57242 nucleic acid expression or 57242 polypeptide activity, thereby identifying a compound capable of treating a metabolic disorder characterized by aberrant 57242 nucleic acid expression or 57242 polypeptide activity.

48. The method of claim 47, wherein the metabolic disorder is a disorder associated with aberrant lipogenesis.

49. The method of claim 47, wherein the disorder is a disorder associated with aberrant lipolysis.

50. The method of claim 47, wherein the disorder is obesity.

51. The method of claim 47, wherein the disorder is diabetes.

52. The method of claim 47, wherein the ability of the compound to modulate the activity of the 57242 polypeptide is determined by detecting the induction of an intracellular second messenger.

53. A method for treating a subject having a metabolic disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression comprising administering to the subject a 57242 modulator, thereby treating said subject having a metabolic disorder.

54. The method of claim 53, wherein the 57242 modulator is a small molecule.

55. The method of claim 53, wherein the metabolic disorder is a disorder associated with aberrant lipogenesis.

56. The method of claim 53, wherein the disorder is a disorder associated with aberrant lipolysis.

57. The method of claim 53, wherein the metabolic disorder is obesity.

58. The method of claim 53, wherein the metabolic disorder is diabetes.

59. The method of claim 53, wherein said 57242 modulator is administered in a pharmaceutically acceptable formulation.

60. The method of claim 53, wherein said 57242 modulator is administered using a gene therapy vector.

61. The method of 53, wherein the 57242 modulator is capable of modulating 57242 polypeptide activity.

62. The method of claim 53, wherein the 57242 modulator is an anti-57242 antibody.

63. The method of claim 53, wherein the 57242 modulator is a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

64. The method of claim 53, wherein the 57242 modulator is a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

65. The method of claim 53, wherein the 57242 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

66. The method of claim 53, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

67. The method of claim 66, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

68. The method of claim 66, wherein the 57242 modulator is a ribozyme.

69. The method of claim 66, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

70. The method of claim 66, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

71. The method of claim 66, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

72. A method for identifying a compound capable of modulating an adipocyte activity comprising:

- a) contacting an adipocyte with a test compound; and
- b) assaying the ability of the test compound to modulate the expression of a 57242 nucleic acid or the activity of a 57242 polypeptide;

thereby identifying a compound capable of modulating an adipocyte activity.

73. The method of claim 72, wherein said adipocyte activity is hyperplastic growth.

74. The method of claim 72, wherein said adipocyte activity is hypertrophic growth.

75. The method of claim 72, wherein said adipocyte activity is lipogenesis.

76. A method for modulating an adipocyte activity comprising contacting an adipocyte with a 57242 modulator, thereby modulating said adipocyte activity.

77. The method of claim 76, wherein the 57242 modulator is a small molecule.

78. The method of claim 76, wherein said adipocyte activity is hyperplastic growth.

79. The method of claim 76, wherein said adipocyte activity is hypertrophic growth.

80. The method of claim 76, wherein said adipocyte activity is lipogenesis.

81. The method of claim 76, wherein the 57242 modulator is capable of modulating 57242 polypeptide activity.

82. The method of claim 81, wherein the 57242 modulator is an anti-57242 antibody.

83. The method of claim 59, wherein the 57242 modulator is a 57242 polypeptide comprising the amino acid sequence of SEQ ID NO:2, or a fragment thereof.

84. The method of claim 81, wherein the 57242 modulator is a 57242 polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

85. The method of claim 81, wherein the 57242 modulator is an isolated naturally occurring allelic variant of a polypeptide consisting of the amino acid sequence of SEQ ID

NO:2, wherein the polypeptide is encoded by a nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

86. The method of claim 85, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

87. The method of claim 86, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

88. The method of claim 86, wherein the 57242 modulator is a ribozyme.

89. The method of claim 86, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

90. The method of claim 86, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

91. The method of claim 86, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2 or 5, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

92. A method for treating a subject having a bone disorder characterized by aberrant 57242 polypeptide activity or aberrant 57242 nucleic acid expression comprising administering to the subject a 57242 modulator, thereby treating said subject having a bone disorder.

93. The method of claim 92, wherein the 57242 modulator is a small molecule.

94. The method of claim 92, wherein the disorder is a disorder associated with aberrant osteogenesis.

95. The method of claim 92, wherein the disorder is osteoporosis.

96. The method of claim 92, wherein the disorder is aberrant bone resorption.

97. The method of claim 92, wherein said 57242 modulator is administered in a pharmaceutically acceptable formulation.

98. The method of claim 92, wherein said 57242 modulator is administered using a gene therapy vector.

99. The method of claim 92, wherein the 57242 modulator is capable of modulating 57242 nucleic acid expression.

100. The method of claim 92, wherein the 57242 modulator is an antisense 57242 nucleic acid molecule.

101. The method of claim 92, wherein the 57242 modulator is a ribozyme.

102. The method of claim 92, wherein the 57242 modulator comprises the nucleotide sequence of SEQ ID NO:1 or 3, or a fragment thereof.

103. The method of claim 92, wherein the 57242 modulator comprises a nucleic acid molecule encoding a polypeptide comprising an amino acid sequence which is at least 90 percent identical to the amino acid sequence of SEQ ID NO:2.

104. The method of claim 92, wherein the 57242 modulator comprises a nucleic acid molecule encoding a naturally occurring allelic variant of a polypeptide comprising the amino acid sequence of SEQ ID NO:2, wherein the nucleic acid molecule which hybridizes to a complement of a nucleic acid molecule consisting of SEQ ID NO:1 or 3 under stringent conditions comprising 6X SSC at 45°C, followed by one or more washes in 0.2X SSC, 0.1% SDS at 50-65°C.

## SEQUENCE LISTING

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 White, David

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ttc atc atg gag tgc gcc aat ggc tgg cac gac atc atg ttc cag ctg	702		
Phe Ile Met Glu Ser Ala Asn Gly Trp His Asp Ile Met Phe Gln Leu			
170	175	180	
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Glu Phe Phe Met Pro Leu Gly Ile Ile Leu Phe Cys Ser Phe Lys Ile			
185	190	195	
gtt tgg agc ctg agg cgg agg cag cag ctg gcc aga cag gct cgg atg	798		
Val Trp Ser Leu Arg Arg Gln Gln Leu Ala Arg Gln Ala Arg Met			
200	205	210	215
aag aag gcg acc cgg ttc atc atg gtg gtg gca att gtg ttc atc aca	846		
Lys Lys Ala Thr Arg Phe Ile Met Val Val Ala Ile Val Phe Ile Thr			
220	225	230	
tgc tac ctg ccc agc gtg tct gct aga ctc tat ttc ctc tgg acg gtg	894		
Cys Tyr Leu Pro Ser Val Ser Ala Arg Leu Tyr Phe Leu Trp Thr Val			
235	240	245	
ccc tcg agt gcc tgc gat ccc tct gtc cat ggg gcc ctg cac ata acc	942		
Pro Ser Ser Ala Cys Asp Pro Ser Val His Gly Ala Leu His Ile Thr			
250	255	260	
ctc agc ttc acc tac atg aac agc atg ctg gat ccc ctg gtg tat tat	990		
Leu Ser Phe Thr Tyr Met Asn Ser Met Leu Asp Pro Leu Val Tyr Tyr			
265	270	275	
ttt tca agc ccc tcc ttt ccc aaa ttc tac aac aag ctc aaa atc tgc	1038		
Phe Ser Ser Pro Ser Phe Pro Lys Phe Tyr Asn Lys Leu Lys Ile Cys			
280	285	290	295
agt ctg aaa ccc aag cag cca gga cac tca aaa aca caa agg ccc gaa	1086		
Ser Leu Lys Pro Lys Gln Pro Gly His Ser Lys Thr Gln Arg Pro Glu			
300	305	310	
gag atg cca att tgc aac ctc ggt cgc agg agt tgc atc agt gtg gca	1134		
Glu Met Pro Ile Ser Asn Leu Gly Arg Arg Ser Cys Ile Ser Val Ala			
315	320	325	
aat agt ttc caa agc cag tct gat ggg caa tgg gat ccc cac att gtt	1182		
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Asn Gly Val Ala Leu Cys Gly Phe Cys Phe His Met Lys Thr Trp Lys			
35 40 45			
Pro Ser Thr Val Tyr Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu			

50	55	60
Met Ile Cys Leu Pro Phe Arg Thr Asp Tyr	Tyr Leu Arg Arg Arg His	
65	70	75
Trp Ala Phe Gly Asp Ile Pro Cys Arg Val	Gly Leu Phe Thr Leu Ala	80
85	90	95
Met Asn Arg Ala Gly Ser Ile Val Phe Leu Thr Val Val Ala Ala Asp		
100	105	110
Arg Tyr Phe Lys Val Val His Pro His His Ala Val Asn Thr Ile Ser		
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Thr Arg Val Ala Ala Gly Ile Val Cys Thr Leu Trp Ala Leu Val Ile		
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Leu Gly Thr Val Tyr Leu Leu Leu Glu Asn His Leu Cys Val Gln Glu		
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Thr Ala Val Ser Cys Glu Ser Phe Ile Met Glu Ser Ala Asn Gly Trp		
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His Asp Ile Met Phe Gln Leu Glu Phe Phe Met Pro Leu Gly Ile Ile		
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Leu Phe Cys Ser Phe Lys Ile Val Trp Ser Leu Arg Arg Arg Gln Gln		
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Leu Ala Arg Gln Ala Arg Met Lys Lys Ala Thr Arg Phe Ile Met Val		
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Val Ala Ile Val Phe Ile Thr Cys Tyr Leu Pro Ser Val Ser Ala Arg		
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Tyr Asn Lys Leu Lys Ile Cys Ser Leu Lys Pro Lys Gln Pro Gly His		
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Ser Lys Thr Gln Arg Pro Glu Glu Met Pro Ile Ser Asn Leu Gly Arg		
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Arg Ser Cys Ile Ser Val Ala Asn Ser Phe Gln Ser Gln Ser Asp Gly		
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